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(FILE 'HOME' ENTERED AT 12:08:36 ON 05 APR 2004)

FILE 'DISSABS, 1MOBILITY, AGRICOLA, AQUASCI, BIOTECHNO, COMPENDEX, COMPUAB, CONF, CONFSCI, ELCOM, HEALSAFE, IMSDRUGCONF, LIFESCI, OCEAN, MEDICONF, PASCAL, PAPERCHEM2, POLLUAB, SOLIDSTATE, ADISCTI, ADISINSIGHT, ADISNEWS, ANABSTR, BIOBUSINESS, BIOCOMMERCE, ...' ENTERED AT 12:08:46 ON 05 APR 2004

E 'SAINT-REMY' 'JEAN-MARIE'?/AU E SAINT-REMY JEAN-MARIE?/AU E JACQUEMIN MARC?/AU

WEST Search History

Hide Items Restore Clear Cancel

DATE: Monday, April 05, 2004

Hide?	Set Name	Query	Hit Count
	DB=PGPB	B, USPT, USOC, EPAB, JPAB, DWPI; THES=ASSIGNEE; PLUR=Y	ES; OP=ADJ
	L13	L11 same l4	5
	L12	L11 same l3	2
	L11	hemophilia adj a	839
	L10	L6 same l4	1
	L9	L5 same l4	159
	L8	L5 same l3	8
	L7	L6 same 13	1
	L6	(anti or antibod\$) adj L5	275
	L5	factor adj (VIII or V)	8473
	L4	sepsis or septic or thrombus	36439
No. of the last of	L3	(systemic inflammatory response syendrome) or SIRS	40826
	L2	Jacquemin-marc-\$.in.	4
	L1	'Saint-remy'-'Jean-Marie'-\$.in.	4

END OF SEARCH HISTORY

ANSWER 8 OF 20 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 5

ACCESSION NUMBER: 1999:465724 CAPLUS

DOCUMENT NUMBER: 131:115050

Antibodies against factor VIII in patients with solid TITLE:

tumors. Successful treatment of cancer may suppress

inhibitor formation

Sallah, Sabah; Singh, Paramjeet; Hanrahan, L. Robert AUTHOR(S): CORPORATE SOURCE:

Department Medicine, Division Hematology/Oncology,

Univ. Tennessee, Memphis, TN, 38163, USA

Haemostasis (1998), 28(5), 244-249 SOURCE:

CODEN: HMTSB7; ISSN: 0301-0147

PUBLISHER: S. Karger AG

Journal DOCUMENT TYPE: English LANGUAGE:

In 1995-1998, the authors treated 5 patients with anti-factor VIII antibodies and spontaneous bleeding. All patients had underlying malignant conditions. Initial control of the bleeding episodes and reduction in inhibitor titer was achieved in all patients. Disappearance of factor VIII inhibitor occurred in 3 patients after either resection of the tumor or chemotherapy. Immunosuppression therapy failed to eradicate the antibody in 2 patients with metastatic disease. Antibodies against factor VIII appearing in certain patients may be directly associated with the underlying malignancy, rather than a coincidental finding. Attempts to reduce the titer or eradicate the inhibitor may fail if recognition of the underlying condition is not sought, or an appropriate treatment of cancer is not offered. Antibodies against factor VIII developing in previously healthy individuals constitute the most common spontaneous inhibitors of any clotting factor. Accurate ests. of the incidence of antifactor VIII inhibitors are not available, since some of these antibodies may not be associated with bleeding, or the condition may be misinterpreted as disseminated intravascular coagulation, especially when it is associated with known underlying malignancy. About 50% of anti-factor VIII antibodies developing in the nonhemophilic population occur in otherwise healthy individuals over the age of 50 yr. Other conditions associated with the development of these inhibitors, in decreasing frequency, include autoimmune diseases, peripartum period, lymphoproliferative disorders, solid tumors and reaction to certain medications [1]. Patients with antibodies against factor VIII usually present with spontaneous bleedings involving soft tissues, retropharyngeal or retroperitoneal spaces, intracerebral or other types of serious hemorrhagic episodes. The most common laboratory abnormality is prolongation of PTT and decreased to absent factor VIII activity. Among the most commonly used products to manage patients with bleeding episodes and autoantibodies against factor VIII are high-dose human factor VIII, and inhibitor by-passing agents. Decreasing the inhibitor titer may also be achieved via plasma exchange and immuno-suppression. The formation of factor VIII antibodies in patients with solid tumors in terms of its course, response to treatment, and prognosis has not been addressed. We describe in this article the occurrence and the course of anti-factor VIII antibodies in 5 patients with solid malignancies.

THERE ARE 8 CITED REFERENCES AVAILABLE FOR THIS REFERENCE COUNT: 8 RECORD. ALL CITATIONS AVAILABLE IN T

L6 ANSWER 3 OF 20 CAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2001:70012 CAPLUS

DOCUMENT NUMBER: 135:32107

TITLE: Transient factor VIII inhibitor in a hemophilia

patient after staphylococcal septic shock syndrome Yamamoto, Kazuhiko; Niiya, Kenji; Shigematu, Terunobu;

AUTHOR(S): Yamamoto, Kazuhiko; Niiya, Kenji; Shigematu, Terunobu; Kiguchi, Toru; Takenaka, Katsuto; Shinagawa, Katsushi;

Ishimaru, Fumihiko; Ikeda, Kazuma; Shima, Midori;

Harada, Mine

CORPORATE SOURCE: Second Department of Medicine, Okayama University

Medical School, Okayama, 700-8558, Japan

SOURCE: International Journal of Hematology (2000), 72(4),

517-519

CODEN: IJHEEY; ISSN: 0925-5710 Carden Jennings Publishing

DOCUMENT TYPE: Journal LANGUAGE: English

PUBLISHER:

concentrate

AB We report a transient type I factor VIII inhibitor that arose in a 30-yr-old hemophilia patient just after staphylococcal septicemia. This situation usually occurs early in the course of substitution therapy with factor VIII concentrate in hemophilia patients. Although disseminated intravascular coagulation and acute respiratory distress syndrome developed after septic shock, the patient recovered following i.v. administration of antibiotics (meropenem and gentamycin), an antithrombin preparation, high-dose methylprednisolone, and recombinant factor VIII

(rFVIII). During this therapy, however, activated partial thromboplastin time gradually lengthened. On the seventh day of hospitalization, intracranial hemorrhage occurred with right hemiplegia, even though the substitution therapy had continued at the same dosage (30 U/kg per day) of rFVIII. At that point, 4 Bethesda units of the type I inhibitor against factor VIII were detected in the plasma. Increased amts. (46 U/kg per day) of rFVIII and prednisolone were administered, and hypothermic therapy was initiated. Following these treatments, the patient's general condition gradually improved, and within 25 days the inhibitor titer dropped to undetectable levels and did not recur during treatment. These clin. findings suggest that the staphylococcal septic shock may have acted as a trigger in the development of transient factor VIII inhibitor in this patient.

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GenCore version 5.1.6
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OM protein - protein search, using sw model	April 5, 2004, 13:36:42 ; Search time 12.824 Seconds (without alignments) 575.678 Million cell update	US-10-044-569B-8 738 1 METPAQLLFLLLWLPDTTGTKVBIKRTVAAPSVFIFPPS 143	BLOSUM62 Gapop 10.0 , Gapext 0.5
OM protein - pr	Run on: '	Title: Perfect score: Sequence:	Scoring table:

Total number of hits satisfying chosen parameters:

389414 segs, 51625971 residues

Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

Issued Patents AA:*
11. (GGT2_6/ptodata/2/iaa/5A_COMB.pep:*
22. /GGT2_6/ptodata/2/iaa/5B_COMB.pep:*
33. /GGT2_6/ptodata/2/iaa/6A_COMB.pep:*
44. /GGT2_6/ptodata/2/iaa/6B_COMB.pep:*
55. /GGT2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
66. /GGT2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
67. /GGT2_6/ptodata/2/iaa/PCTUS_COMB.pep:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

*	Appl	Appl	Appl	Appl	Appli	Appl	Appl	Appli	Appli	App1	Appl	Appl	Appl	Appl		•	•		, App	Appl	Appli	Appl	Appl	Appl	Appl	Appl	Appl
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Length	235	235	233	233	150	234	234	134	129	226	226	226	226	224	226	116	116	116	116	226	234	226	224	224	224	224	235
% Query Match	90.3	90.3	88.7	88.7	88.0	87.4	87.4	81.8	79.1	77.9	77.4	77.4	77.1	76.8	76.7	76.4	76.4	76.4	76.4	76.4	75.9	75.7	75.1		74.9	74.4	73.8
Score	666.5	666.5	654.5	654.5	649.5	645	4	604	583.5	575	571	571	569	567	566	564	564	564	564	564	560	559	554	553	553	549	545
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US-09-535-832A-17 US-08-472-087-88 US-08-472-087-21 US-09-472-087-23 US-09-472-087-93 US-08-772-087-93 US-08-172-087-93 US-08-172-087-93 US-08-199-575-153 US-08-199-575-153 US-08-1089-1087-108 US-08-108-108-108-108-108-108-108-108-108-	
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ALIGNMENTS

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61 PGGAPRLLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSALLTF 120
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Sequence 14, Application US/09472087

Sequence 14, Application US/09472087

Batent No. 6682736

GENERAL INFORMATION:

APPLICANT: HANSON, DOUGLAS C.

APPLICANT: MUSUU, MARK J.

APPLICANT: MUSULER, EILLEN E.

APPLICANT: GILMAN, STEVEN C.

APPLICANT: GILMAN, JOSE R.

APPLICANT: CORVALAN, JOSE R.

APPLICANT: CORVALAN, JOSE R.

APPLICANT: DAVIS: C. GEOFFREY

APPLICANT: DAVIS: US/09/472,087

FILE REFERENCE: ASK. PFL

CURRENT FILING DATE: 1999-12-23

FRIOR PILING DATE: 1998-12-23

FRIOR FILING DATE: 1998-12-23

FRIOR FILING DATE: 1998-12-3

FRIOR FILING DATE: 1998-12-3
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Patent No. 6682736;
GENERAL INFORMATION:
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: NEVEU, MARK J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
CORGANISM: Homo sapiens
US-09-472-087-14
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US-09-472-087-65
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61 PGQAPRLLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSALLTF 120
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US-08-862-124-5
US-08-862-124-5
Sequence 5, Application US/08862124

APPLICANT: Dain, Michael D.
APPLICANT: Matti, Pradip K.
APPLICANT: Matti, Pradip K.
APPLICANT: Matti, Pradib K.
APPLICANT: SEQUENCES.
TITLE OF INVENTION: SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCOL TITLE OF INVENTION: DETECTION OF CANCERS
TITLE OF INVENTION: DETECTION OF CANCERS
NUMBER OF SECUENCES: 28
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 METPAQLLFLLLLWLPDTTGEIVLTQFPGTLSLSPGERATLSCRASQSVASAYLAWYQQK
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88.7%; Score 654.5; DB 4; Length 233;

Best Local Similarity 91.6%; Pred. No. 1.8e-54;

Matches 131; Conservative 2; Mismatches 7; Indels 3
                                                                                                                                                                                                                                                            APPLICANT: HANGOVALION:
APPLICANT: HANGOV, DOUGLAS C.
APPLICANT: HANGOV, MARK J.
APPLICANT: MUELLER, EILLEN E.
APPLICANT: HANGE, JEFFREY H.
APPLICANT: HANGE, JEFFREY H.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: CROVALAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABX-PF1
CURRENT FALLING DATE: 1999-12-23
FRIOR PRILING DATE: 1999-12-23
PRIOR PRILING DATE: 1999-12-23
PRIOR PRILING DATE: 1999-12-23
PRIOR PRILING DATE: 1998-12-23
SOFTWARE: PATENTING OF SEC ID NOS: 147
SOFTWARE: PATENTING OF SEC ID NOS: 147
SOFTWARE: PATENTING DATE: 2.1
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STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
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                                                   118 GGGTKVEIKRTVAAPSVFIFPPS 140
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Parent No. 6682736
GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEBR PC compatibl
OPERATING SYSTEM: PC-DOS/N
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CORGANISM: Homo sapiens
US-09-472-087-67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: MAYEU, TAKEN U.
APPLICANT: HUBLLER, EILLEN E.
APPLICANT: HUBLLER, JEFFREY H.
APPLICANT: HONUS, UEFFREY H.
APPLICANT: GANGAM, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILLE REFERENCE: ABX. PF1
CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT APPLICATION NUMBER: 60/113,647
PRIOR APPLICATION WHERE: 60/113,647
PRIOR PILLING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 147
SOFFWARE: PALENTIN UM.
             APPLICANT: HANKE, JEFFREY H.
APPLICANT: GILMAN STEVEN C.
APPLICANT: DAVIS, C. GEOFFREY
APPLICANT: CORVALAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REPRESENCE: ABX.PF1
CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION WHEBER: 601113,647
PRIOR PILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PATENTIN US: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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Patent No. 6682736
GENERAL INFORMATION
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: NEVEU, MARK J.
MUELLER, EILLEN E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-15
                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
US-09-472-087-65
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Best Local Similarity
Matches 131; Conserv
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LENGTH: 233
                                                                                                                                                                                                                                                                                                                     SEQ ID NO 65
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ENCODING THE

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Sequence 69, Application US/09472087 Patent No. 6682736
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ZIP: 53717-1914
COMPUTER READBLE FORM:
MDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatibl
OPERATING SYSTEM: PC-DOS/W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens
US-09-472-087-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                       Patent No. 6682736
GENERAL INFORMATION:
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STATE: WI
                                                                                                                                                                                                                                                                                                       US-09-472-087-69
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Matches 130;
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US-08-405-034-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 PGQAPRLLIYGASTRATGMPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPQTPQ 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 METPAQLIFILLIMIPDTTGEIVLTQFPGTLSLSPGERATLSCRASQSVASAYLAWYQQK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 MEFQAQLLFLLLLMLPDITGDIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQK 64
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APPLICANT: HANSON, DOUGLAS C.
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: MUSEU, MARK J.
APPLICANT: MUSEU, MARK J.
APPLICANT: GILMAN, SIFVEN C.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: GOLVALAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABS.-PP1
CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT FILING DATE: 1998-12-23
PRIOR FILING DATE: 1998-12-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 234;
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Pred. No. 1.4e-53;
2; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
Patentin Release #1.0, Version #1.30
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88.0%; Score 649.5; DB 3;

Best Local Similarity 87.7%; Pred. No. 3.2e-54;

Matches 128; Conservative 7; Mismatches 8;
                 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/862,124
FILING DATE: 22-ARY-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 31,943
REFERENCE/DOCKET NUMBER: 31,943
RELEPRA: (650) 494-0792
TELEPRA: (650) 494-0792
TELEPRA: (650) 494-0792
TELER: 706141
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
LENGTH: 150 amino acids
TYPE: Amino Amino acids
TYPE: Amino Amino acids
TYPE: Amino 
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Patent No. 6682736
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Best Local Similarity 90.9%;
Matches 130; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 147
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
CRGANISM: Homo sapiens
US-09-472-087-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 유
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60 PGOAPRPLINGVSSRATGIPDRESGSGTDFTLTISRLEPEDFAVYYCQQYGISP-FTF 118
60 PGQAPRPLIYGVSSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYCQQYGISP-FTF 118
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Patent No. 5744585

Patent No. 5744585

Patent No. 19744585

APPLICANT: Madenica, Rajko D.
APPLICANT: Mikerjee, Sonjoy

TITLE OF INVENTION: Human Monoclonal Antibody Against Lung

TITLE OF INVENTION: Carcinoma

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dewitt Ross & Stevens, S.C.

STREET: 8000 Excelsior Drive, Suite 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87.4%; Score 645; DB 4; Length 234; 90.9%; Pred. No. 1.4e-53; Live 2; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: HANSON, DOUGLAS C.
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: NUELER, EILLEN E.
APPLICANT: HANKE, JEFREY H.
APPLICANT: GILMAN, SIEVEN C.
APPLICANT: GILMAN, SIEVEN C.
APPLICANT: CORVALAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFRENCE: ARX-PF1
CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 6/113,647
PRIOR PILITING DATE: 1998-12-23
NUMBER OF SEQ. ID NOS: 117
SOFTWARE: PATENTIN USE: 2.1
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                                                                                                     121 GGGTKVEIKRTVAAPSVFIFPPS 143
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                                                                                                                                                                    119 GPGTKVDİKRTVAAPSVFİFPPS 141
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61 PGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRVEPEDFAVXYCQQXDNS-VCTF 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 METPAQLIFILIMIPDITGEIVITQSPGTLSLSAGERATLSCRASQSVSSRYLAWYQQK
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Pred. No. 4.6e-48;
4; Mismatches 9; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 42, Application US/09456090A

Patent No. 6680209

GENERAL INPORMATION:
APPLICANT: Buschler, Joe
APPLICANT: Valkirs, Gunars
APPLICANT: Caray, Jeff
APPLICANT: Lonberg, Nils
TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
FILE REFERENCE: 020015-000200US
CURRENT APPLICATION NUMBER: US/09/456,090A
CURRENT FILIG DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 110
SOFTWARE: Patentin Ver. 2.1
LENGTH: 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 226,
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Best Local Similarity 90.2%; Pred. No. 5.7e-47;
Matches 111; Conservative 6; Mismatches 6; Indels
                                  41450-FWC-DIV
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 41
TELECOMUNICATION INFORMATION:
TELEFRONE: 617-523-3400
TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 89.2%;
Matches 116; Conservative
                                                                                                                                       TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
OCHANISM: Homo sapiens
CTHER INFORMATION: M1-5L
US-09-456-090A-42
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US-09-456-090A-42
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15-08-48-47-47-47

Patent No. 5852186

GENERAL INFORMATION:

APPLICANT: MARASCO, Wayne A.

APPLICANT: SOURCEST, JOSEPHO G.

APPLICANT: POSNER, Marshall R.

TITLE OF INVENTION: REACTIVE NEUTRALIZING HUMAN

TITLE OF INVENTION: AND USE THEREOF

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSE: DIKE, BRONSTEIN, ROBERTS & CUSMAN, LLP

STREET: 130 Water Street

COUNTRY: USA

COUNTRY: USA

COUNTRY: USA

CONPUTER: IBM COMPATIBLE

COMPUTER: IBM COMPATIBLE

FILING DATE: 0'-UN-1995

CLASSIFICATION NUMBER: 0'-UN-1995

FILING DATE: 0'-UN-1995

RILING DATE: 0'-UN-1995

PRILING DATE: 0'-DEC-1991

ATTORNEY APPLICATION NUMBER: 0'-DEC-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 PGQAPSLLIYGASTRATGIPDRFSGSGSGTDFILTISRLEPEDFAVYYCQQYGSSARYIF 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 81.8%; Score 604; DB 1; Length 134; Best Local Similarity 88.1%; Pred. No. 5.5e-50; Matches 118; Conservative 6; Mismatches 10; Indels
  SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/405,034
                                                                             FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,492
REFERENCE/POCKET NUMBER: 34656.009
TELEPHONE: 608-831-2106
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 134 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                     : 134 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-405-034-4
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141 PPS 143
                     121 PPS 123
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       Sequence 50, Application US/09456090A; Batent No. 6680209; GENERAL INFORMATION:
APPLICANT: Buechler, Joe
APPLICANT: Usechler, Gunars; APPLICANT: Usechler, Joe
TITLE OF INVENTION: APPLICANT: Usechler, Joe
TITLE OF INVENTION: US/09/456,090A; UNIS; TILE REFERENCE: 02005-0002
CURRENT APPLICATION NUMBER: US/09/456,090A; CURRENT FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 110
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 86, Application US/09456090A

Patent No. 6680209

GENERAL INFORMATION:
APPLICANT: Buechler, Joe
APPLICANT: Gray, Jeff
APPLICANT: Gray, Jeff
APPLICANT: Gray, Jeff
APPLICANT: Groberg, Nils
APPLICANT: Groberg, Nils
TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
FILE REPRENCE: 02015-002000000
CURRENT APPLICATION NUMBER: US/09/456,090A

CURRENT APPLICATION NUMBER: 1999-12-06
NUMBER OF SEQ ID NOS: 110

SOFTWARE: PATENTIN VET: 2.1

TEMBER OF SEQ ID NOS: 120

SEQ ID NO 86

TEMBER OF SEQ ID NOS: 120

TEMBER OF SEQ ID NOS: 110
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77.4%; Score 571; DB 4; Length 220
Best Local Similarity 91.1%; Pred. No. 1.4e-46;
Matches 112; Conservative 4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 571; DB 4; Length 22 Pred. No. 1.4e-46; 4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 91.1%;
Matches 112; Conservative
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OCANISM: Homo sapiens
COTHER INFORMATION: M2-33L
US-09-456-090A-86
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CTHER INFORMATION: M1-23L
US-09-456-090A-50
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US-09-456-090A-86
US-09-456-090A-50
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81 HRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSALLTFGGGTKVEIKRTVAAPSVFIF 140
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Sequence 52, Application US/09456090A

Patent No. 6680209

GENERAL INPORMATION:

APPLICANT: Buschler, Gunars

APPLICANT: Valkirs, Gunars

APPLICANT: Unberg, Nils

TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS

FILE REFERENCE: 020015-000200US

CURRENT APPLICATION HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS

FILE REFERENCE: 1999-12-06

CURRENT APPLICATION UNSER: US/09/456,090A

CURRENT FILING DATE: 1999-12-06

SOCTHARE: PatentIN Ver. 2.1

SEQ ID NO 52

LENGTH. 224
                                                                                                                                                         GENERAL INPORATION:
APPLICANT: BUGGLIE', Joe
APPLICANT: Buchler, Joé
APPLICANT: Buchler, Jéff
APPLICANT: Cary, Jéff
APPLICANT: Cary, Nils
ITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
FILE REFERENCE: 020015-00020003
CURRENT APPLICANTON NUMBER: US/09/456,090A
CURRENT FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 110
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 80
LENGTH: 226
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Pred. No. 2.1e-46;
6; Mismatches 7; Indels
US-09-456-090A-80
; Sequence 80, Application US/09456090A
; Patent No. 6680209
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89.48;
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OCANISM: Homo sapiens
TOTHER INFORMATION: M2-20L
US-09-456-090A-80
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TYPE: PRT; OCTABLE STATE OF STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE 
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81 HRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSALLTFGGGTKVEIKRTVAAPSVFIF 140

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81 HRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSALLTFGGGTKVEIKRTVAAPSVFIF 140
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61 NRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSS--FTFGPGTKVDIKRTVAAPSVFIF 118
                                                                                                                                                                                                                                                                                                                                                                                                                                         21 BIVLTOFPGTLSLSPGERATLSCRASOSVASAYLAWYQQKPGQAPRLLIYGASSRATDIP 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EIVWTQSPGTLSLSPGERATLSCRASQGVSSSYLAMYQQKPQQAPRLLIYGASSRATGIP 60
                                                                                Query Match 76.7%; Score 566; DB 4; Length 226; Best Local Similarity 89.4%; Pred. No. 4e-46; Matches 110; Conservative 5; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: April 5, 2004, 13:44:09 Job time: 12.824 secs
                                                                                                                                                                                                                                                                                                                        TYPE: PRT
OCANISM: Homo sapiens
CTHER INFORMATION: M2-11L
US-09-456-090A-72
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

April 5, 2004, 13:25:01; Search time 12.1827 Seconds (without alignments) 1184.358 Million cell updates/sec

US-10-044-569B-2 788 Title: Perfect score:

1 MDWTWRILFLVAAATGTHAQ.......MVTVSSASTKGPSVFPLGSR 150 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues Searched:

Total number of hits satisfying chosen parameters:

283366

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	DB ID	1 2 S23623 I	5 2 S31600 Ig heavy	5 2 S49530 ant	7 2 S14683 Ig mu	0 2 PL0105 anti-PR2 ery	2 2 S31596 Ig heavy	3 2 S29257 Ig heavy chain V	7 2 S18551 Ig heavy	7 2 S31680 Ig heavy chain V	7 1 HVHU35 Ig heavy	2 2 S19245 Ig heavy chain pr	7 2 S18553 Ig heavy chain	3 2 PN0538 Ig heavy chain V	3 1 ElHUND Ig heavy chain pr	7 2 S18552 Ig heavy chain	7 1 HVHUHG IG heavy	1 2 S21924 Ig heavy chain	1 2 PL0011 Ig heavy	4 2 S21916 Ig heavy chain		2 2 A32483 Ig heavy	2 2 A32483 Ig heavy chain 8 2 S26911 Ig heavy chain	2 2 A32483 Ig heavy chain 8 2 S26911 Ig heavy chain 9 2 S37483 Ig gamma-2a cha	2 2 A32483 Ig heavy cha 8 2 226911 Ig heavy cha 9 2 S37483 Ig gamma-2a 4 1 G2MS11 Ig gamma-2a	2 2 A32483 Ig heavy chain 8 2 S26911 Ig heavy chain 9 2 S37483 Ig gamma-2a cha 1 G2MS11 Ig gamma-2b cha 7 2 P70371 Ig gamma-chain	2 2 A32483 Ig heavy chain 9 2 526911 Ig heavy chain 9 2 537483 Ig gamma-2a cha 4 1 G2MS11 Ig gamma-2b cha 7 2 PT0371 Ig pamma chain 7 2 C41287 Ig heavy chain	2 2 A32483 Ig heavy chain 9 2 526911 Ig heavy chain 9 2 S37483 Ig gamma-2a cha 4 1 G2MS11 Ig gamma-2b cha 7 2 P70371 Ig gamma chain 7 2 C41287 Ig heavy chain 0 2 PNO44	2 2 A32483 Ig heavy chain 8 2 526911 Ig heavy chain 9 1 G2MS11 Ig gamma-2b cha 7 2 PT0371 Ig gamma chain 7 2 C41287 Ig heavy chain 8 2 S01321 Ig heavy chain 9 2 PN0444 Ig heavy chain 9 2 S01321 Ig gamma-2b cha	2 2 A32483 Ig heavy chain 9 2 526911 Ig heavy chain 9 2 537483 Ig gamma-2b cha 1 G2MS11 Ig gamma-2b cha 7 2 770371 Ig pamma-chain 0 2 PN044 Ig heavy chain 0 2 DN044 Ig pamma-2b chain 1 2 JL0076 Ig heavy chain
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chain	chain	chain	chain	chain	chain	chain	chain	chain	chain	chain	chain	chain	chain	chain	chain
heavy	heavy	gamma	heavy	heavy	heavy	heavy	heavy	heavy	heavy	heavy	heavy	heavy	heavy	heavy	gamma
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116	116	178	118	138	126	139	117	86	128	135	123	129	131	136	246
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18.5	418.5	417.5	416.5	416	415	414.5	414	413	412.5	411.5	409	409	407	407	407
4															

ALIGNMENTS

RESULT 1

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Ig heavy chain V region precursor - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Caccession: 823621
R;Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, D.A.;
J. Exp. Med. 175, 831-842, 1992
A;Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from A;Reference number: 823623; MUID:92158804; PMID:1740665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Modecule type: DNA
A;Modecule type: DNA
A;Residues: 1-171 < ColE>
A;Cross-references: EMBL:X59702; NID:g32010; PIDN:CAA42223.1; PID:g32011
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heteroctetramer; immunoglobulin homology
F;34-117/Domain: immunoglobulin homology < IMM>
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	1,	09	09	117	120		
	9; Gaps	WVGQAP	MVRQAP	CAV	CALEYF		
171;	9	TELPVH	TAYOMH	VYYYY	DTAVYY		
Length	Indels	KVSGYTL	KGSGYTF	SLSSLRSD	LSRLTSD		
DB 2; e-41;	24;	GASVKVS	GASVKVS	STDIAYM	SISTAYM	FPL 147	PPL 156
580.5; No. 1.9	smatches	SGAEVKKP	GAEVKKP	SVIMTADI	tyritrbr	ASTKGPSV	STKGPSV
Score Pred.	10; Mis	AQVQLVQS	SOVOLVOS	YAREFOGS	YGQKFQGB	TMVTVSS	TMVTVSS
73.78;	tive	AAATGTH	AAATGAH	PESGESI	IPNSGGTG	AFDIWGOG	/FDIWGQG
Query Match 73.7%; Score 580.5; DB 2; Length 171; Best Local Similarity 72.4%; Pred, No. 1.9e-41;	Matches 113; Conservative 10; Mismatches 24;	1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP 60	DWTWRILFL	61 GKGLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYCAV 117	QGLEWMGWIR	118PDPDAFDIWGQGTMVTVSSASTKGPSVFPL 147	121 YDGSDLKPSDVFDIWGGGTMVTVSSASTKGPSVFPL 156
tch al Si	113;	Ή.	-E	61 6	61 6	118 -	121 Y
Query Ma Best Loc	Matches	δλ	qq	δλ	q	δλ	q
		J	ы	O.	ы	•	\Box

RESULT 2
31600

19 heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Jour, 1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: 331600
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
Bubmitted to the EMBL Data Library, June 1992
A;Reference number: 331585
A;Accession: 331600
A;Accession: 331600
A;Accession: 331600
A;Accession: 331600
A;Residues: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-136 cCulp.
A;Cross-references: EMBL:Z14165; NID:G30994; PIDN:CAA78534.1; PID:G30995
C;Superfamily: immunoglobulin V region; immunoglobulin homology

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A, McCoule type: mRNA
A, Residues: 1-160 <s11.5
A, Note: the authors translated the codon GAC for residues 108 and 109 as Glu
A, Note: the authors translated the codon GAC for residues 108 and 109 as Glu
C, Comment: The antibody is one of the cold agglutinins that preferentially bind red blo
C, Superferanily: immunoglobulin V region; immunoglobulin homology
C, Keyvords: autoantibody; hemagglutinin
F;1-15/Domain: immunoglobulin homology xIMM>
F;34-117/Domain: immunoglobulin homology xIMM>
F;59-84/Region: complementarity-determining 1
F;69-84/Region: complementarity-determining 2
F;18-131/Domain: D region cAGG>
F;118-131/Domain: C region cAGG>
F;145-160/Domain: C region cAGG>
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C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
S;Cousinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the A;Reference number: S31596
A;Accession: S31596
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: PL0105
R;Silberstein, L.E.; Litwin, S.; Carmack, C.E.
d; Exp. Med. 169, 1631-1643, 1989
A;Title: Relationship of variable region genes expressed by a human B cell lymphoma sec A;Reference number: PL0106; MUID:89235583; PMID:2541221
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                                                                                                                                                                                                                                                                                                                                                                                              61 GQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYXCAKTGI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 GKGLEWVGSFDPESGESIYAREFQGSVTMTADISTDIAYMELSSLRSDDTAVYYCA-VP- 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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C;Species: Homo sapiens (man)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 26-Apr-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MDWTWSILFLVAAATGAHSQVQLVASGAEVNKPGASVKVSCKASGYTFTSYGISWVRQAP
                                                                                                                                                                                                                                                      1 MDWTWRFLFVVAAATGVQSQVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAP
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                                                                        Length 627;
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                                                                                                                                        31; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------DPDAFDIWGOGTMVTVSSASTKGPSVFPLGS 149
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                                                                    64.5%; Score 508; DB 2;
llarity 61.2%; Pred. No. 8.5e-35;
Conservative 17; Mismatches 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63.8%; Score 503; DB 2;
63.4%; Pred. No. 5.2e-35;
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F;34-117/Domain: immunoglobulin homology <IMM>
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Matches 102; Conservative
                                                                Query Match
Best Local Similarity
Matches 101; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CiAccession: S49530
RyMahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
RyMahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
Rymahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
Rymahmoudi, M.; Edwards, J.; Cairns, Cotober 1994
A;Description: Molecular characterization of natural human anti-Sm autoantibodies.
A;Recession: S49530
A;Status: preliminary
A;Status: preliminary
A;Residues: 1-135 <MAH>
A;Residues: 1-135 <MAH>
Cisuperfemences: EMBL: Z46348; NID:g560839; PIDN:CAA86467.1; PID:g560840
Cisuperfemily: immunoglobulin V region; immunoglobulin homology <IMM>
Cisuperfemily: immunoglobulin homology <IMM>
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C;Species: Homo sapiens (man)
C;Dacte: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 23-Jul-1999
C;Accession: S14683; S08047
R;Friedlander, R.M.; Nussenzweig, M.C.; Leder, P.
Nucleic Acids Res. 18, 4278, 1990
A;Title: Complete nucleotide sequence of the membrane form of the human IgM A;Reference number: S14683; MUID:90332450; PMID:2115996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Species: Homo sapiens (man)
Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                          1 MDWTWRILFLVAAATSAHSQVQLVQSGAEVKKPGASVKVSCRASGYTFTSYDINWVRQAT
                                                                                                                                                                                                                                                          1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELFVHWVGQAP
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A; Residues: 1-627 «FRI»
A; Residues: 1-627 «FRI»
A; Cross-references: EMBL:X17115; NID:g33450; PIDN:CAA34971.1; PID:g33451
C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: immunoglobulin; membrane protein
F;1-15/Domain: signal sequence #status predicted «SIG»
F;16-627/Product: Ig mu chain #status predicted «MAI»
                                                                                                                                                                                  1;
                                                                                                             Length 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 135;
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                                                                                                          DB 2;
                                                                                                                                                                              12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or DM1/JH4b)
                                                                                                      Query Match

Best Local Similarity 74.3%; Pred. No. 2.7
Matches 101; Conservative 12; Mismatches
   C;Keywords: heterotetramer; immunoglobulin F;34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      anti-Sm antibody VH chain (VH1/DK1
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120 TGYNYWQQGTLVTVSS 135
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Matches 100; Conserv
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Cypecies: Home states (man)
Cyspecies: A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
Submitted to the ENBi Data Library, June 1992
A,Description: Mechanisms that generate human immunoglobulin diversity operate from the A,Reference number: 831885
A,Reference number: 831885
A,Reference number: 831886
A,Reference number: B1885
A,Residues: 1-17 <CUI>
A,Molecule type: manA
A,Residues: 1-17 <CUI>
C,Genetics: EMBL:Z14213; NID:g37795; PIDN:CAA78582.1; PID:g37796
C,Genetics:
A;Introns: 16/1
C,Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <INM>
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C;Species: Homo sapiens (man)

C;Species: Homo sapiens (man)

C;Accession: S00476; S34013

C;Accession: S00476; S34013

S;Matsuda, F.; Lee, K.H.; Nakai, S.; Sato, T.; Kodaira, M.; Zong, S.Q.; Ohno, H.; Fukuh EMBO, 7, 1047-1051, 1988

A;Title: Dispersed localization of D segments in the human immunoglobulin heavy-chain l A;Reference number: S00476; MUID:88296408; PMID:2841108
   J. Exp. Med. 175, 831.842, 1992
A,Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors A,Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors A,Reference number: S23623; MUID:92156804; PMID:1740665
A,Rocession: S23625
A,Rolecule type: DAA
A,Residues: 1-117 < OLE>
A,Residues: 1-117 < OLE>
A,Cross-references: EMBL:X59704; NID:g32552; PIDN:CAA42225.1; PID:g32553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MDWIWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP
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                                                                                                                                                                                                                                                                                                                           A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heteroterramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-117/Product: Ig heavy chain V region (VI-2) #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>
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75.9%; Pred. No. 2.5e-32;
iive 10; Mismatches 18;
Lu, E.W.; Huang, D.F.; Soto-Gil,
. 175, 831-842, 1992
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Best Local Similarity 75.9<sup>3</sup>
Matches 88; Conservative
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nes 90; Conserv
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Cristian V region precursor (VI-2) - human (fragment)
Cristian 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999
Cristian 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999
Cristian 21851; S23625
Rrishin, E.K.; Matsuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; Ismino, E.K.; Matsuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; Ismino, E.K.; Matsuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; Ismino, E.K.; Matsuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; Ismino, E.K.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; Ismino, E.K.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; Ismino, E.K.; Nagaoka, H.; Pulino, I.; PID:1937832
A; Rocession: S1851
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Cipate: 22-Nov-1993 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
Cipate: 22-Nov-1993 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
Cipate: 22-Nov-1993 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
Cipate: J. Biochan. 2071 1115-1121, 1992
A. Title: Molecular characterization of a human anti-Rh(D) antibody with a D(A; Reference number: S29257; MUID:92362614; PMID:1499555
A. Status: preliminary
A. Status: preliminary
A. Molecular type: DNA
A. Residues: 1-148 < CHO>
A. Residues: 1-148 < CHO>
A. ChOoper references: GB:542403; NID:g253699; PIDN:AAB22940.1; PID:g253700
Cisuperfemily: immunoglobulin V region; immunoglobulin homology
F;34-117/Domain: immunoglobulin homology < INM>
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                               A;Residues: 1-132 <CUI>
A;Residues: 1-132 <CUI>
A;Cross-references: EMBL:Z14166; NID:G30996; PIDN:CAA78535.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterocetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                    Query Match 61.0%; Score 480.5; DB 2; Best Local Similarity 69.9%; Pred. No. 3.2e-33; Matches 95; Conservative 11; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60.4%; Score 476; DB 2;
62.2%; Pred. No. 8.5e-33;
ive 14; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chain V region precursor - human (fragment)
s: Homo sapiens (man)
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Best Local Similarity 62.2
Matches 92; Conservative
A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
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Ig heavy chain V region precursor (VI-3b) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Ja.Jan-1995 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999
C;Accession: S18553; S26916
R;Shin, E.K.; Matsuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; Rshin, E.K.; Matsuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; A;Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: c
A;Reference number: S18551; MJID:92037524; PMID:1935893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 21-Jan-2000
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 21-Jan-2000
C;Accession: PNO538
R;Avila, M.A.; Vazques, J.; Danielsson, L.; de Cossio, M.E.F.; Borrebaeck, C.A.K.
A;Avila, M.A.; Vazques, J.993
A;Title: Sequence determination of variable region genes of two human monoclonal antibo
A;Reference number: PNO535; MUID:93273246; PMID:8500770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A) residues: L-117 <SHI>
A) residues: L-117 <SHI>
A) for solution: L-117 <SHI>
A) for solution: SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = SHI = 
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A;Residues: 1-138 <AVI>
A;Residues: 1-138 <AVI>
A;Cross-references: GB:M97804; NID:g185373; PIDN:AAB18935.1; PID:g1669777
A;Note: the authors translated the codon CCA for residue 75 as Ser, GCC for residue C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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C;Keywords: heterotetramer; immunoglobulin
F;I-1900cmain: signal sequence #statutus predicted'<SIG>
F;20-117/Product: Ig heavy chain V region (VI-3b) #status predicted
F;34-117/Domain: immunoglobulin homology <IMM>
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C,Species: Homo saniene (man)
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                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Accession: S18553
A, Status: translation not shown
A, Molecule type: DNA
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Best Local Similarity
Matches 90; Conserv
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C;Species: Homo sapiens (man)
C;Date: 22.Nov-1933 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: 519245
R;Kirkham, P.M.; Mortari, F.; Newton, J.A.; Schroeder, H.W.
R;Kirkham, P.M.; Mortari, F.; Newton, J.A.; Schroeder, H.W.
A;Kirkham, P.M.; Mortari, F.; Newton, J.A.; Schroeder, H.W.
A;Keference number: 819245; MUID:92164649; PMID:153739
A;Accession: 519245
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                   A, Molecule type: DNA
A, Residues: 1-117 < MATS>
A, Cross-references: EMBL:X07448; NID:g33104; PIDN:CAB56703.1; PID:g6002173
A, Note: the authors translated the codon AGT for residue 89 as Met
B, Mariette, X.; Taapis, A.; Brouet, J.C.
Eur. J. Immunol. 23, 846-851, 1993
A, Fitle: Nucleotidic sequence analysis of the variable domains of four huma
A, Reference number: S34001; MUID:93209281; PMID:7681398
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A;Map position: 14q32.33-14q32.33
A;Introns: 16.7
A;Introns: 16.7
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-17/Pomain: signal sequence #status predicted <SIG>F;20-117/Product: Ig heavy chain V region (V35) #status predicted <MAT>F;34-117/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 464; DB 1; Length 117;
Pred. No. 6.6e-32;
8; Mismatches 20; Indels
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Matches 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 20-116 <MAR>
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Best Local Similarity
Matches 86; Conserv
A; Accession: S00476
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Search completed: April Job time: 12.1827 secs
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EIHUND

Ig heavy chain precursor V-I region (Nd) - human (fragments)

C.Species: Homo sapiens (man)

C.Species: Homo sapiens (man)

C.Date: 31-Mar-1981 #sequence_revision 05-Apr-1983 #text_change 21-Jan-2000

C.Date: 31-Mar-1981 #sequence_revision 05-Apr-1983 #text_change 21-Jan-2000

C.Date: 31-Mar-1981 #sequence_revision 05-Apr-1983 #text_change 21-Jan-2000

R.Kenten, J.H.; Molgaard, H.V.; Houghton, M.; Derbyshire, R.B.; Viney, J.; Bell, L.O.; G

R.Kenten, J.H.; Molgaard, H.V.; Houghton, M.; Derbyshire, R.B.; Viney, J.; Bell, L.O.; G

R.Kersence number: A93933 MulD:83065234; PMID:681566

A.Reference number: A93933 MulD:83065234; PMID:681566

A.Residues: 1-143 <a href="Mailto:Res">Res</a>
A.Residues: 1-143 <a href="Mailto:Res">Res</a>
R.Bennich, H.H.; Johansson, S.G.O.; Von Bahr-Lindstrom, H.

In Immediate Hypersensitivity: Modern Concepts and Developments, Bach, M.K., ed., pp.1-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C,Genetics:
A,Gross-references: GDB:128528, OMIM:147070
A,Gross-references: GDB:128528, OMIM:147070
A,Gross-references: GDB:128528, OMIM:147070
A,Map position: 14432.33-14432.33
C;Superfamily: immunoglobulin V region; immunoglobulin, pyroglutamic acid
C;Keywords: heterotetramer; immunoglobulin; pyroglutamic acid
C;Keywords: heterotetramer; immunoglobulin, pyroglutamic acid
F;1.15-00main: signal sequence Hstatus predicted <MAT>
F;3.0-113/Domain: immunoglobulin homology <IMM>
F;3.0-113/Domain: immunoglobulin homology <IMM>
F;3.0-111/Disulfied site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimen F;3.7-111/Disulfide bonds: #status experimental
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Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: Ja-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999
Cistocession: 81852
Rishin, E.K.; Matsuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; H
Smbo J. 10, 3641-3645, 1991
A;Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: cl
A;Reference number: $18551; MUD:92037524; PMD:1935893
A;Accession: $18552
A;Accession: $18552
A;Accession: $18552
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A;Accession: $117 < SML:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GHGLEWVGWINDNSGGTNYAPRFQGRVTMTRDASFSTAYMDLRSLRSDDSAVFYCAKSDP 116
     61 AQKFQGRVTMTEDTPTDTASLELSRVRSEDTAVYYCVTGPPRLSELAIFGVVKRIRGPFD 120
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C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
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A,Contents: annotation; partial sequence
A,Note: this epsilon chain was isolated from a myeloma protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 -----DAFDIWGQGTMVTVSS 136
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                                                                                                      125 IWGQGTMVTVSSASTKGP
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Res 90; Conserv
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F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-117/Product: Ig heavy chain V region (VI-3) #status predicted <WAT>
F;20-117/Domain: immunoglobulin homology <IMM>
Cuery Match
S6.9$; Score 448; DB 2; Length 117;
Best Local Similarity 73.3$; Pred. No. 1.4e-30;
Matches 85; Conservative 11; Mismatches 20; Indels 0; Gaps 0;
Matches 85; Conservative 11; Mismatches 20; Indels 0; Gaps 0;
Oy | IMDWTWRILPLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP 60
Db | IMDWTWRILPLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAMHWVRQAP 60
Oy | GGCLEWVGSFPESCESTYAREFGGSVTWTADTSTDIAYMELSSLRSDMAVYCA 116
Db 61 GQRLEWMGANSNAGNGNTKXSGEPGGSVTTTRDTSASTAMBLSSLRSEDMAVYCA 116
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5, 2004, 13:43:01

homo sapien homo sapien homo sapien homo sapien caiman croc mus musculu carassius a homo sapien homo sapien homo sapien

P01769 P01773 P01773 P01765 P01765 P01765 P01761 P01813

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP
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SEQUENCE FROM N.A. ubMed=2841108;
MEDLINE=88296408; PubMed=2841108;
Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q.,
Ohno H., Fukuhara S., Honjo T.;
Ohno H., Fukuhara S., Honjo T.;
Thispersed localization of D segments in the human immunoglobulin heavy-chain localization of D segments in the human immunoglobulin heavy-chain locals.";
EMBO J. 7:1047-1051(1988).
-1- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IG HEAVY CHAIN V-I REGION V35. IG-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58.9%; Score 464; DB 1; Length 11 ilarity 75.9%; Pred. No. 1.5e-36; Conservative 8; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 117
117 AA; 13009 MW; BE61CE63F8CE97BD CRC64;
                                                                                                                                                                                                                                                                          HVIG HUMAN

ID HVIG HUMAN

STANDARD; PRT; 117 AA.

P23083;

DT 01-NOV-1991 (Rel. 20, Last sequence update)

DT 10-OCT-2003 (Rel. 20, Last sequence update)

DT 10-OCT-2013 (Rel. 42, Last annotation update)

DF 10-OCT-2013 (Rel. 42, Last annotation update)

OF 10-NOV-1991 (Rel. 42, Last annotation update)

OF 10-NOV-1991 (Rel. 42, Last annotation update)

OF 10-NOV-1991 (Rel. 42, Last annotation update)

OF 10-NOV-1991 (Rel. 42, Last annotation update)

OF 10-NOV-1991 (Rel. 42, Last annotation update)
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PIR; S00476; HYHU35.
HSSP, P01772; 2FB4.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005823; F:antigen binding; NAS.
GO; GO:0006955; P:inmune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR007596; Ig-v.
InterPro; IPR007596; Ig-v.
INTERPRO; IPR007596; Ig-v.
INTERPRO; IPR007596; Ig-v.
INTERPRO; SM00406; IGv; 1.
PR05TTE; PS50835; IG_LIKE; 1.
SIGNAL
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20 117 IG_HRAVY CHAIL
                          HV31_HUMAN
HV03_CARAU
HV31_HUMAN
HV35_HUMAN
HV35_HUMAN
HV35_HUMAN
HV35_HUMAN
HV37_HUMAN
HV37_HUMAN
117
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                                                                                                       April 5, 2004, 12:10:21; Search time 6.85279 Seconds (without alignments) 1139.758 Million cell updates/sec
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                                                                                                                                                                   US-10-044-569B-2
788
1 MDWTWRILFLVAAATGTHAQ.......MVTVSSASTKGPSVFPLGSR 150
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                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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length: 2000000000
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HV07_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.; (In) Bach M.K. (eds.); Immediate hypersensitivity: modern concepts and developments, pp.1-36, Marcel Dekker, New York (1978).

-!- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 GKGLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYYCAVPDP
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GKGLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYYCA 116
                           GQGLEWMGRINDNSGGTNYAQKFQGRVTSTRDTSISTAYMELSRLRSDDTVVYYCA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-83065234; PubMed-6815656; Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J., Bell L.O., Gould H.J.; Cloning and sequence determination of the gene for the human immunoglobulin epsilon chain expressed in a myeloma cell line."; Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
                                                                                                                                                                                                                                                                                                                      Bukaryoča, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Signal; Pyrrolidone carboxylic acid.
SIGNAL 1 19
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IG-LIKE.
PYRROLIDONE CARBOXYLIC ACID.
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GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005853; F:antigen binding; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             147 AA; 16491 MW; 948F9F72A5366C20 CRC64;
                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
19 heavy chain V-I region ND precursor (Fragments).
Homo sapiens (Human).
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IH -> HI (IN REF. 2).
VG -> GV (IN REF. 2).
MISSING (IN REF. 2).
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                                                                                                                                                          STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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RESULT 3

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
PubblinE=81144028; PubMed=6298778;
Rebiavi G., Ram D., Glazer L., Zakut R., Givol D.;
"Evolutionary aspects of immunoglobulin heavy chain variable region
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                              21-JUL-1986 (Rel. 01, Created)
1-JUL-1986 (Rel. 01, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
1g heavy chain V-I region HG3 precursor.
If hemo sapiens (Human).
Eukaryota, Metazoa; Chordaes, Craniata, Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
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117 AA
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GO; GO:0005576; C:extracellular; NAS.

GO; GO:0003825; F:antigen binding; NAS.

GO; GO:0006855; P:immune response; NAS.

InterPro; IPR007110; IG-like.
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PROSITE, PS50835, IG LIKE; 1.
Immunoglobulin V region; Signal.
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PIR; A02024; HVHUHG.
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Pfam; PF00047; ig; 1
SMART; SM00406; IGv;
PROSITE; PS50835; IG
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SECUENCE FROM N.A.
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120 PDAFDIWGQGTMVTVSS 136
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Best Local Similarity 57.75
Matches 79; Conservative
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                                                                                                                                                                                                                                                                                                                                              NCBI TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           NON TER
SEQUENCE
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ID HV48 MOU
AC P03980;
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                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMED outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by, and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GKGLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYYCAVPD- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GRGLEWIGRIDPNSGGTKYNEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCARYDY 120
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                                            "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Gaps
                                                                              MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDON MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL (NPB ANTIBODIES).
          MEDLINE=81234548; PubMed=6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.
Baltimore D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musimae; Mus
                                                                                                                                                                                                                                                                                                                                                        IG HEAVY CHAIN V REGION B1-8/186-2. RAPAÜWORK-1. COMPLEMENTARITY-DETERMINING-1. FRAMIEWORK-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 139;
                                                                                                                                                                                                                                                                                                                                                                                                     COMPLEMENTARITY-DETERMINING-2. FRAMEWORK-3. D SEGMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 52.6%; Score 414.5; DB 1; Length Best Local Similarity 57.6%; Pred. No. 7.5e-32; Matches 80; Conservative 17; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15419 MW; 1B57DD4FD0C9F465 CRC64;
                                                                                                                                                                                                                                                                                      Interrio, ...
Pfam; P800047; ig; 1.
PROSITE; P850835; IG_LIKE; 1.
PROSITE; P850835; IG_LIKE; 1.
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21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1999 (Rel. 38, Last annotation update)
Ig heavy chain V region S43 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   137 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 -- PDAFDIWGQGTMVTVSS 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 YGSSYFDYWGQGTTLTVSS 139
                                                                                                                                                                                                                                               PDB; 1A6U; 27-WAX-98.

PDB; 1A6W; 15-JUL-98.

INTERPRO; 1PR007110; Ig-like.

InterPro; IPR005596; Ig_V.

Pfam; PF00047; ig; 1.
                                                                                                                                                                                                                         EMBL; J00529; AAA38170.1;
PIR; A90809; MHMS18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              139 AA;
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SEQUENCE FROM N.A.
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NON TER
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation
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                                                                                                      "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-87(1991).
-!- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOW! MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL (NPB ANTIBODIES).
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MEDLINE=84248078; PubMed=6429663;
Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
MEDLINE-81234548; PubWed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
Baltimore D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-OCT-1986 (Rel. 02, Created)
23-OCT-1986 (Rel. 02, Last sequence update)
15-UL-1999 (Rel. 38, Last annotation update)
15-UL-1999 (Rel. 38, Last annotation update)
1g heavy chain V region TEPC 1017 precursor.
Mus musculus (Mouse)
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
D SEGMENT.
JHZ SEGMENT.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51.6%; Score 406.5; DB 1
57.7%; Pred. No. 4.1e-31;
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NON TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GKGLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYYCAVPDP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Gaps
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MEDLINE=81234548; PubMed=6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.
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                           llegitimate recombination generates a class switch from C mu to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Created)
15-JUL-19986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last amocation update)
16 heavy chain V region 102 precursor.
18 heavy chain V region 102 precursor.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; 
                                                                                                                                                                                                                                                                                                                                     IG HEAVY CHAIN V REGION TEPC 1017
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COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 50.3%; Score 396; DB 1; Length 138; Best Local Similarity 55.1%; Pred. No. 4e-30; Matches 76; Conservative 20; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPLEMENTARITY-DETERMINING-3. FRAMEWORK-4.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15576 MW; 748157E4C6907B8E CRC64;
                                              delta in an IgD-secreting plasmacytoma.";
Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 117 AA.
                                                                                             PIR, A02033, HVMST7.
HSSP, P01810, 2FBJ.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596, Ig-v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Signal.
SIGNAL.
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SMAAT; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V regIon; Signal.
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InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               138 AA;
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P01750;
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"Heavy chain variable region contribution to the NPb family of antibodies : sometic mutation evident in a gamma 2a variable region.";

"I at 124.625-637(1981).

"I ELLI 24.625-637(1981).

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MEDLINE=81234548; PubMed=6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI TaxID=10090;
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                                FRAMEWORK-1.
COMPLENENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLENENTARITY-DETERMINING-2.
FRAMEWORK-3.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                              Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPLEMENTARITY-DETERMINING-1.
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COMPLEMENTARITY-DETERMINING-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31; Indels
IG HEAVY CHAIN V REGION 102.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31; Indels
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                                                                                                                                                                                                                                                                                                                                      740A65DD851FCA8C CRC64;
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ilarity 59.5%; Pred. No. 3.7e-28;
Conservative 16; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
47.5%; Score 374; DB 1;
Best Local Similarity 59.0%; Pred. No. 3.7e-28;
Matches 69; Conservative 17; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HV09 MOUSE STANDARD; PRT; 117 AA. P01753; P11271; 21-UUL-1986 (Rel. 01, Created) 01-UUL-1989 (Rel. 11, Last sequence update) 15-UUL-1999 (Rel. 38, Last annotation update) 19 heavy chain V region 186-1 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRAMEWORK-3.
BY SIMILARITY.
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Best Local Similarity
Matches 69; Conserv
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HV04 MOUSE
P01748;
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SEQUENCE
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STATE SOURCE STATE STATE SOURCE STATE SOURCE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    д
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MGWSCIIFFLVATATGVUSQVQLQQSGPEVVRPGVSVKISCKGSGYTFTDYAMHVKQSH 60
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                                                GRGLEWIGRIDPNSGGTKYNEKFKSKATLTVDTSSSTAYMQLHSLTSEDSAVYYCA 116
                       61 GKGLEWVGSFDPESGESIYAREFQGSVTMTADISTDIAYMELSSLRSDDTAVYYCA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=82222262; PubMed=6806821;
Knapp M.R., Liu C.-P., Newell N., Ward R.B., Tucker P.W., Strober S.,
Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Simultaneous expression of immunoglobulin mu and delta heavy chains by a cloned B-cell lymphoma: a single copy of the VH gene is shared by two adjacent CH genes.";

Proc. Natl. Acad. Sci. U.S.A. 79:2996-3000(1982).
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IG HEAVY CHAIN V REGION BCL1. IG-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47.3%; Score 373; DB 1; Length 13.
52.9%; Pred. No. 5.5e-28;
ive 20; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15078 MW; 6827CFBC6DB3F35E CRC64;
                                                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                        V region BCL1 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; PO1772; 2FB4.
InterPro; IPROO7110; IG-like.
InterPro; IPRO0310; IG-like.
Pfam; PF00047; ig; 1.
SWART; SWOO406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                      21-JUL-1986 (Rel. 01, Created)
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121 NYFDYWGQGTTLTVSS 136
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Best Local Similarity 52.9
Matches 72; Conservative
                                                                                                                                                                                        STANDARD;
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135
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                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
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136 AA;
                                                                                                                                                                                                                                                                                                           g heavy chain
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ID HV02 MOUSE
AC P01746;
                                                                                                                                                                                     MOUSE
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SEQUENCE
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140 AA.

PRT;

STANDARD;

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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41; Indels 4;
                                                                                                                                                                                                                                                  MEDLINE=82152818; PubMed=6801765;
Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
Capra J.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 140;
                                                                                                                                                                                                                                                                                                                                              "Somatic mutation in genes for the variable portion of the finanuoglobulin heavy chain."; Science 216:303-311(1982) -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IG HEAVY CHAIN V REGION 93G7. IG-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15514 MW; 25A4CBBE31DA5CE8 CRC64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46.8%; Score 369; DB 1;
50.0%; Pred. No. 1.3e-27;
iive 25; Mismatches 41;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last Sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
19 heavy chain V region 9367 precursor.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
heavy chain V region 23 precursor.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117 AA.
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PIR; A94264; HVMSG7.
HSSP; PO1810; 2FBJ.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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nes 70; Conservative
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                                                                                                    Mus musculus (Mouse)
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SEQUENCE FROM N.A.
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                                                                                                                                                                             NCBI_TaxID=10090;
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MOUSE
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                                                                                                 "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981).
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                      AEDLINE=81234548; PubMed=6788376;
Sothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1998 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
15 havy chain V region VHSS8 B4 precursor.
Mus musculus (Mouse).
Eukariotai Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musines; Mus.
                                                                                                                                                              -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES. PIR; A02030; HVMS23. HSSP; P01810; 2FBJ.
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Yancopoulos G.D., Alt F.W.;
"Developmentally controlled and tissue-specific expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IG HEAVY CHAIN V REGION 23.
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 117;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30; Indels
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; Pred. No. 3.2e-27;
18; Mismatches 30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRAMEWORK-3
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Cell 40:271-281(1985).
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                                                                                                                                                                                                                                                                                InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46.2%;
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HSSP; P01810; 2FBJ.
InterPro; IPR007110; Ig-like.
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117
117 AA;
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P06328;
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SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gapa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GRGLEWIGNIDPNSGGTKXNEKFKSKATLTVDKPSSTAXMQLSSLTSEDSAVYYC 115
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
MCBI_TaxID=10090;
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MEDLINE=81245215; PubMed=6789211;
Givol D., Zakut R., Effron K., Rechavi G., Ram D., Cohen J.B.;
Givol D., Zakut R., Effron K., Rechavi G., Ram D., Cohen J.B.;
Notersity of germ-line immunoglobulin VH genes.";
Nature 292:426-430(1981).
-1- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                   B4.
                                                                                                                                                                                            IG HEAVY CHAIN V REGION VH558
PRAMEMORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 117;
                                                                                                                                                                                                                                                                                                                                     COMPLEMENTARITY-DETERMINING-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12834 MW; B8862FAC67ABD345 CRC64;
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; Pred. No. 7.6e-27;
17; Mismatches 32;
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10-0CT-2003 (Rel. 42, Last annotation update)
19 heavy chain V region 108A precursor.
IGH-VJ558.
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SWART; SM00406; IGV; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
SIGNAL
Pfam; PF00047; ig; 1.
SMART; SM0406; iGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
SIGNAL
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57.4%;
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Best Local Similarity
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                                                1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP 60
                                                                "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981).
-!- MISCELLANBOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED: GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
                                                                                                                GKSLEWIGYIYPYNGGTGYNQKFKSKATLTVDNSSSTAYMELSSLTSEDSAVYYCA 116
                                                                                                 61 GKGLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYYCA 116
                         Gaps
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                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebzata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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llarity 57.8%; Pred. No. 2.2e-26;
Conservative 15; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IG HEAVY CHAIN V REGION 145.
PRAMENORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMENORK-2.
  Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPLEMENTARITY - DETERMINING - 2
Query Match
45.2%; Score 356; DB 1; Length 11
Best Local Similarity 55.2%; Pred. No. 1.8e-26;
Matches 64; Conservative 20; Mismatches 32; Indels
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                                                                                                                                                                                     HV10 MOUSE STANDARD; PRT; 117 AA. P01754; P11270; Created) 01-JUL-1986 (Rel. 01, Created) 01-JUL-1989; (Rel. 11, Last sequence update) 28-FES-2003 (Rel. 41, Last annotation update) 1G heavy chain V region 145 precursor.
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PKSP; PO1810; ZPBJ.
MGD; MGI:96486; Igh-VJ558.
InterPro; IPR007110; Iglike.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; ISNRT; SWOR406; IGV; I.
PROSITE; PS50835; IG_IKE; I.
                                                                                                                                                                                                                                                                                                                                                      STRAIN=C57BL/6;
MEDLINE=81234548; PubMed=6788376;
                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
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SEQUENCE
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Best Local
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"Heavy chain variable region contribution to the NPD family of antibodies: somatic mutation evident in a gamma 2a variable region."; cell 24:625-637(6981).

-1- MISCELLANEOUS: THIS GERMINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.

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                                              1 MGWSCIMLFLAATATGVHFQVQLQQPGAELVKPGASVKLSSKASGYTFTSYWMHWVKQRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-81234548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
Baltimore D.;
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
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COMPLEMENTARITY-DETERMINING-2.
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                                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
19-FEB-2003 (Rel. 41, Last annotation update)
19 heavy chain V region 3 precursor.
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MGD; MGI:96486; IGh-VJSS8.
InterPro; IPR007110; IG-like.
InterPro; IPR003596; IG_V.
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                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=C57BL/6;
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P01749;
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Search completed: April 5, 2004, 13:24:55 Job time: 7.85279 secs

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0727ps homo sapien
096gs6 homo sapien
09brv0 homo sapien
08wy24 homo sapien
088424 homo sapien
095978 homo sapien
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Q8Vdc9 mus n
Q99la6 mus n
Q92lx1 mus n
Q99lc4 mus n
Q99lc5 mus n
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                       - protein search, using sw model
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1: Sp archea:*
2: Sp_bacteria:*
3: Sp_fungi:*
4: Sp_human:*
1: Sp_human:*
1: Sp_mammal:*
1: Sp_mammal:*
1: Sp_nammal:*
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Gapop 10.0 , Gapext 0.5
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	Q8k0z4 mus Q9lwtl mus Q9lwtl mus Q9lwrl mus		Q7tmt6 mus Q91wt3 mus Q8vcx4 mus Q924r0 mus	0924r4 mus 0924r1 mus 0924r5 mus 091vaz mus 0924r7 mus	167 Q914/67 mus musculu	ALIGNMENTS
Q99L3 Q9UL95 Q9UL92					091V67 0924P7 0924Q9 0924Q7 0924Q3 0924R3 0924R6	AI
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Gaps
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MEDLINE=98322155; PubMed=9657749;
Jacquemin M.G., Vander Elst L.P.L.;
Jacquemin M.G., Vander Elst L.P.L.;
Jacquemin and kinetics of factor VIII inactivation: study with an IgG4 monolonal antibody derived from a hemophilia A patient with inhibitor.";
                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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16031 MW; 563D164AB22802D5 CRC64;
                                                                                           Last sequence update)
Last annotation update)
                                    150 AA
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                                                    Q9Y298;
01-NOV-1999 (TrEMBLrel. 12, Created
01-NOV-1999 (TrEMBLrel. 12, Last se
01-OCT-2003 (TrEMBLrel. 25, Last an
IGG VH protein precursor (Fragment)
IGG VH.
                                      PRT;
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                                      PRELIMINARY;
                                                                                                                                                                 Homo sapiens (Human)
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Matches 150, Conserv
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PROSITE; PS50835; IG LIKE; 5.
PROSITE; PS00290; IG MHC; 3.
                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
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Best Local Similarity 66.0%
Matches 101; Conservative
                                                                                                                   PRELIMINARY;
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SEQUENCE 614 AA;
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WEDLINE-22388257; PubMed=12477932;

WEDLINE-22388257; PubMed=12477932;

A Strausberg R.L., Peingold B.A., Grouse L.H., Derge J.G.,

A Altaschil S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschil S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hsieh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hsieh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

A Villalon D.K., Murny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

R. Helton B.K., Ketteman M., Madan A., Gibbs R.A.,

A Hakesley R.M., Touchman J.W., Green B.D., Dickson M.C.,

R. Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

R. Kzzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

R. Reeneration and initial analysis of more than 15,000 full-length human
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                                                                1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP
                                                                                                                 GKGLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYYCAVPDP
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.; Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases. Submitted (APR-2003) 12. 1; ... Hypothetical protein. SEQUENCE 469 AA; 51395 MW; C8D5BB12BAAF795C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                     469 AA.
                                                                                                                                                                                                                                            DAFDIWGQGTMVTVSSASTKGPSVFPLGSR 150
                                                                                                                                                                                                                DAFDIWGQGTMVTVSSASTKGPSVFPLGSR 150
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                                                                                                                                                                                                                                                                                                                                                                                                                         OLT-2003 (TERMELTE) 25, C. 01-0CT-2003 (TERMELTE) 25, La Hypochetical protein. Homo sapiens (Human).

Eukaryota, Metaan.
                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY; -6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 67.3%
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                             Q7Z7P5
Q7Z7P5;
01-OCT-2003
01-OCT-2003
01-OCT-2003
                                                                                                                                                                                                                                                            121
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Query Match

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61 GKGLEWVGSFDPESGESIYAREFQGSVTMTADISIDIAYMELSSLRSDDTAVYYCA--- 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MDWTWRILFLVAAATDAYSQMQLVQSGAEVKKTGSSVKVSCKASGYTFTYRYLHWVRQAP
                                                                                                                                                                                                                                                                                            Strausberg R.;
Strausberg R.;
Submitted (UUL.2001) to the EMBL/GenBank/DDBJ databases.
EMBL, BC009851, AAH09851.1;
PIR, 815590, 815590.
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0005522; C:intracellular; IEA.
GO; GO:0003150; P:transcription of transcription, DNA-dependent; IEA.
InterPro; IPR000005; HTAArac.
InterPro; IPR0001006; HTAArac.
InterPro; IPR00110; Ig_MRc.
InterPro; IPR001596; Ig_W.
PF00047; ig; S.
SMART; SM00406; IGV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 614;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31; Indels
                                                                                       Homo sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Butele
Mammalia; Buteria; Primates; Catarrhini; Hominidae; Homo
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Prostate;
Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC005951; AAH05951.1; -.
HSSP; P01789; IMCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67921 MW; 55EF536E77AA9BBB CRC64;
Last sequence update)
Last annotation update)
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Last annotation update)
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66.0%; Pred. No. 3.6e-39;
ive 17; Mismatches 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        149
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PRELIMINARY;
                                                                                                                                                                                                                        Mus musculus (Mouse)
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SMART; SM00406; IG
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GKGLEWVGSFDPESGESIYAREFQGSVTWTADTSTDIAYMELSSLRSDDTAVYYCA--- 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GKGLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYYCAVPD- 119
                                                                                                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                                                                                                                                                                                                1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MDWTWSILFLVAAATGAQSQVHLVQSGAEVMSPGASVRVSCKTSGYAFHTYSIIWVRQAP
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                            11;
                                                                                                                                                                                                                                                                            Length 500;
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                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00047; ig; 4.
SMART; SM00406; IGV; 1.
PROSITE; PS50029; IG_MHC; 4.
PROSITE; P$500290; IG_MHC; 1.
SEQUENCE 497 AA; $3665 MW; F24D08DFASA663E5 CRC64;
                                                                                                                                                                                                                      0A9BF43F2A3CC6D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---VPDPDAF----DIWGQGTMVTVSSASTKGPSVFPL 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SYSSCQNDYYYYYMDVWGKGTTVTVSSASPTSPKVFPL 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                   Query Match 60.7%; Score 478.5; DB 4; Best Local Similarity 60.8%; Pred. No. 2.5e-36; Matches 96; Conservative 13; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----PDAFDIWGQGTMVTVSSASTKGPSVFPL 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          497 AA
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InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; Ig; 4.
SWART; SM00406; IGV; 1.
PROSITE; PS00835; IG_LIKE; 4.
PROSITE; PR00290; IG_MHC; 1.
Hypothetical protein.
SEQUENCE 500 AA; 54154 MW; 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 57.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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Q8WY24
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Kawai U., Shinagawa A., Shibata K., Yoshino M., Itch M., Ishii Y., Arakawa T., Hara A., Shibata K., Yoshino M., Itch M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Komo H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyoswa H., Kondo S., Yamanaka I., Asito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Rieschmann W., Gasaterland T., Gissi C., King B., Kochiwa H., A., Schrim L., S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schrim L., Staubli F., Suzuki R., Tomita M., Magner D., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Pujita M., Gariblid M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monbaerts P., Nordone P., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Schombach C., Sakamoto N., Narabihaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Nasahi, V., Wasahi, V., Kawaji H., Kohtsuki S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP
                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00406; ĪĠv; 1.
PROSITE; PSS0835; IG LIKE; 4.
PROSITE; PS00290; IG MHC; 1.
SEQUENCE 473 AA; $1699 MW; 9DED57A514475PBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
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Last annotation update)
  473 AA.
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PRT;
                                                                                                                                                                                                                                                                                                                                                          STRAIN=C57BL/6J; TISSUE=Pancreas; MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MACLE AKO0718; BA225349.1; -
PIR; S26746; S26746.
HSSP; P01842; 7FAB.
MGD; MGI:96443; Igh-1.
InterPro; IPR007110; Ig-like.
InterPro; IPR007100; Ig-MHC.
InterPro; IPR003596; Ig-WHC.
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17,
25,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 57.7%;
                                                  01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 409:685-690(2001)
                                                                                                                                   1810060009Rik protein.
IGH-1 OR 1810060009RIK.
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01-MAY-1999
01-OCT-2003
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095978
ID 095978;
AC 095978;
DT 01-MAY-DT 01-0CT-3
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61 GHGLEWIGEILPGSGSTNYNEKFKGKATFTADTSSNTAYMQLSSLTSEDSAVYYCARRLG 120
                                                                                                                                                    61 GKGLEWYGSPDPESGESIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYYCAVP-D 119
                                                                                                                             61 GKGLEWVGSFDPESGESIYAREFQGSVTMTADISTDIAYMELSSLRSDDTAVYYCAVPDP 120
                                           1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSGKVSGYTLTELPVHWVGQAP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MDWTWRILFLVAAATGTHAQVQLVQSGABVKKPGASVKVSCKVSGYTLTELPVHWVGQAP
                                                                           1 MDWIWRVFCLLAVGFGAHSQVQLVQSGAEVKKPGASVKVSCKASGYIFSNYYMNWVRQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13; Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IGG2A.
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56.5%; Score 445.5; DB 11; Length 613; 57.3%; Pred. No. 3.9e-33; Live 20; Mismatches 43; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R. 1
Strausberg R. 1
Strausberg R. 2
Submitted (DEC-2011) to the EMBL/GenBank/DDBJ databases.
EMBL, BC018315, AAH1815.1; -
MGD, MGI:96448; Igh-6.
R. InterPro; IPR07710; Ig-11ke.
R. InterPro; IPR003006; Ig WHC.
R. InterPro; IPR003596; Ig_v.
R. Fam; PF0047; Mg; 5.
RNART; SM00406; IGv.
RPCSITE; PS50835; IG_LIKE; 5.
RPCSITE; PS50835; IG_LIKE; 5.
RPCSITE; RS00290; IG_MHC; 3.
RPGSITE; RS00290; IG_MHC; 3.
Indels
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1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Anti-MOG 212 variable gamma 2a (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
  36;
                                                                                                                                                                                                               121 DAF-----DIWGOGTMVTVSSASTKGP 142
                                                                                                                                                                                                                                                          121 ITPGGAVSKGFYYYGMDVWGQGTTVTVSSHPRPAP 155
  17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 PDAFDIWGOGTMVTVSSASTKGPSVFPLGS 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 RWYPDVWGAGTTVTVSSESOSFPNVFPLVS 150
                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                 PRT;
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(TrEMBLrel, 20, L
(TrEMBLrel, 25, L
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    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE=Salivary gland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein.
IGH-6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                   08VCX7;
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2002
01-OCT-2003
    89;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 GKGLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYYCA--- 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C TISSUE-Peripheral blood;
A JOX A., Zander T., Kueppers R., Irsch J., Kanzler H., Kornacker M.,
A JOX A., Zander T., Kueppers R., Irsch J., Kanzler H., Kornacker M.,
Bohlen H., Diehl V., Wolf J.;
"Absence of immunoglobulin in Hodgkin-Reed Sternberg cells of a
IT maked cellularity Hodgkin's disease is associated with
T somatic mutations within the untranslated regions of rearranged and
RT somatic mutations within the untranslated regions of rearranged and
RT Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
BR MEB; AJ005570; CAA06599.1; -.
BR HSSP; P01772; 2FB4.

BR InterPro; IPR007110; Ig-like.
BR InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Homo sapiens putative microfibrillar protein with Ig-like domain 3 mRNA (Matrix Cell Adhesion Molecule-3, Mat-CAM 3).";

MRNA (Matrix Cell Adhesion Molecule-3, Mat-CAM 3).";

Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AY039025; AAK82649.1; -..

InterPro; IPR007110; Ig-like.

Ffam; PF00047; ig; 1.

SMART; SMO0405; ig/v.

PROSITE; PS00805; IG_LIKE; 1.

SEQUENCE 159 AA; 17497 NW; 5D29537E881FAF02 CRC64;
                                               Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 58.9%; Score 464; DB 4; Length 15 Best Local Similarity 59.6%; Pred. No. 1.3e-35; Matches 90; Conservative 17; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 21 POTENTIAL.
157 157
157 AA: 17304 MW; 86986EDDA84D88B5 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 WRSGNYNGHWGQGTPVTVSSSSTKGPSVFPL 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Putative matrix cell adhesion molecule-3.
Homo sapiens (Human).
    VH1 protein precursor (Fragment)
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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Best Local Similarity
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Tilson M.D.;
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EMBL; BC028249; AAH28249.1;
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PIR, PH1142, PH1142.
PIR, PH1149, PH1149.
PIR, PH1150, PH1150.
PIR, PH1151, PH1151.
PIR, PH1152, PH1152.
                                                                                                                                                                                                                                                                                                                                 F33932; F33932
PH1105; PH1105
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Best Local Similarity
                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                    PH1128;
PH1131;
PH1134;
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PH1126;
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Q8K172;
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                                                                                                                                                                                                                                                                                                                                               61 GHGLEWIGELLPGSGRINYNEKFKGKTTFTADTSSNTAYIQFSSLTSEDSAVYYCANYGS 120
                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                      1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP 60
                                                                                                                                                                                                                                                                                          1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP
                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                               Query Match 56.5%; Score 445; DB 11; Length 168; Best Local Similarity 55.7%; Pred. No. 8.3e-34; Matches 83; Conservative 21; Mismatches 43; Indels 35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003495; AAH03495.1;
PIR; R33922, F33932.
R HSSP; POL810; 2FBJ.
R InterPro; IPR007110; Ig-like.
R InterPro; IPR003066; Ig-WC.
R PERM; PR00047; Ig-V.
R PROSITE; PS0835; IGV; 1.
R PROSITE; PS0835; IG-LIKE; 4.
R PROSITE; PS00290; IG-MC; 2.
                                                                                                                         Targeting T cells to the CNS.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
BMBL; AJ416332; CAC94687.1;
InterPro; PR00110; Ig-like.
InterPro; IPR001110; Ig-like.
Fam: PF00047; Ig: 1.
SMART: SM00406; Ig: 1.
PR051TE; PS0635; IG'; ILE; 1.
NON_TER.
                                                     STRAIN=BALB/c;
Chernajovsky Y.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                               NON TER 168 168 NON TER 168 AA; 18293 MW; 1E3719FCCOE72723 CRC64;
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484 AA; 52567 MW; BEAEA4F9BCF582FA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                    [2]
SEQUENCE FROM N.A.
STRAIN=BALB/c;
                                        SEQUENCE FROM N.A.
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SEQUENCE 46
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AC 0991A
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61 GKGLKWAWAVNIETGESVYADDFKGRFAFSLETSASTIHLQINNLKNEDTATYFCARSDY 120
                                                                         61 GKGLEWYGSFDPESGESIYAREPQGSVTMTADTSTDIAYMELSSLRSDDTAVYYCAVPDP 120
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1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP
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1-0cr-2002 (TrEMBLrel. 22, Last sequence update)
01-0cr-2003 (TrEMBLrel. 25, Last annotation update)
similar to expressed sequence A1893S85.
Mus musculus (Mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE=Breast tumor;
Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
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InterPro; IPR003597; Ig cl.
InterPro; IPR003596; Ig cl.
InterPro; IPR003596; Ig v.
InterPro; IPR003596; Ig v.
InterPro; IPR00407; Ig; 4.
SMART; SM00406; IGv; 1.
PROSITE; PS06085; IG LIKE; 4.
PROSITE; PS0608290; IG MR; 2.
BRQUENCE 482 AA, 52121 NW; A06FP083E771D084 CRC64;
                                                                                                                                                                              D----AFDIWGOGTMVTVSSASTKGPSVFPL 147
                                                                                                                                                                                                        121 DYDIYAMDYWGQGTSVTVSSESARNPTIYPL 151
                                                                                                                                                                                                                                                                                                                                                      482 AA
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463 AA; 51007 MW; EAA674C6BBC30783 CRC64;
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Best Local Simi:
Matches 81; (
    SEQUENCE
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Q99L25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MGWNCIILFLVATATGVHSQVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Gaps
                                                                                                                                                                                                                                                      092IK1;
01-DEC-2001 (TEMBLE) 19, Created)
01-DEC-2001 (TEMBLE) 19, Last sequence update)
01-DEC-2003 (TEMBLE) 25, Last annotation update)
Hypothetical protein.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 11; Length 278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 55.3%; Score 435.5; DB 11; Length Best Local Similarity 56.7%; Pred. No. 1.2e-32; Matches 85; Conservative 18; Mismatches 44; Indels
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Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databages.
EMBL; BC003435; AAH03435.1; -.
PIR, B45837; B45837.
HSSP; P01842; 7FAB.
MGD; MGI:96446; 1gh-4.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
FIREM: PF00017; Ig; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC012207; AAH12207.1; -
InterPro; IPR007110; Ig-1ike.
InterPro; IPR007156; Ig-v.
Ffan; PF00047; ig; 2.
SWART; SW00406; IGy; 1.
PROSITE; PS50835; IG_IKE; 2.
Hypochetical protein.
SEQUENCE 278 AA; 29778 MW; F894F955DDCD948A CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to RIKEN CDNA 1810060009 gene.
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PROSITE; PSS0835; IG LIKE; 4.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                    PRELIMINARY;
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SEQUENCE FROM N.A.
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Q99LC4;
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61 GQGLEWVGEIYPGSGNTYYSEKFKGKATLTTDKSSSTAYMHLSSLTSEDSAVYFCARSSY 120
                                                                                                                                                                                                             61 GKGLEWYGSFDPESGESIYAREFQGSVTWTADTSTDIAYMELSSLRSDDTAVYYCAVPDP 120
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Q90125,
01-UUN-2001 (TrEMBLrel. 17, Last sequence update)
01-UUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to RIKEN cDNA 1810060009 gene.
Sums musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Mus.
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  DB 11; Length 463;
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A Strausberg R.;

L Submitteed (FEB-2001) to the EMBL/GenBank/DDBJ databases.

R EMBL; BC003889; AAH03888.1; -.

R HSSP, P01842; 7FAB.

R InterPro; IPR007110; Ig-11ke.

R InterPro; IPR003065; Ig_WHC.

R InterPro; IPR0030596; Ig_W.

R FAMR PF00047; ig; 3.

R SWART; SW00466; IGV; 1.

R PROSITE; PSS0835; IG_KHC; 1.

R PROSITE; PSS0835; IG_KHC; 1.

S SEQUENCE 473 AA; 52449 MW; BE9889B7986DA155 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54.8%; Score 431.5; DB 11; Length 52.6%; Pred. No. 5.8e-32; ive 24; Mismatches 42; Indels
S5.1%; Score 434.5; DB 11; Length Similarity 54.0%; Pred. No. 2.9e-32; S1; Conservative 25; Mismatches 41; Indels
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                                                                                                                                                                                                                                                                                                                         121 DAFDI---WGQGTMVTVSSASTKGPSVFPL 147
                                                                                                                                                                                                                                                                                                                                                      473 AA.
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nes 81; Conservative
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us-10-044-569b-2.rag

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein April 5, 2004, 12:09:21 ; Search time 48.4772 Seconds (without alignments) 874.270 Million cell updates/sec Run on:

Title: Perfect score:

US-10-044-569B-2 788 1 MDWTWRILFLVAAATGTHAQ.........WVTVSSASTKGPSVFPLGSR 150 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1586107 Total number of hits satisfying chosen parameters: 1586107 seqs, 282547505 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

A Geneseq 29Jan04:*

1: geneseqp1980s:*

2: geneseqp2000s:*

3: geneseqp2001s:*

5: geneseqp2002s:* 6: geneseqp2003as:* 7: geneseqp2003bs:* geneseqp2004s:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ion	8 Heavy cha	6 Human B02	٠.	2 Human mon		9 Human pol	6 Anti-huma	Human ant	O Human imm	2 Human IGF	4 Monoclona	0 Heavy cha	0 Humanised	6 Human imm	2 Monoclona	5 Humanised	4 Human pol	5 Humanised	3 Humanised	4 Mouse hum	2 Humanised	4 Humanised	3 Mouse hum	6 Humanised	5 Humanised
Description	Aab47058	Aa018876	4	Aay24372	37		Aau74296	Ade28427	Aab3621(Aay96302		Aaw4865(Aar7761(Aar66316	Abu08023	Aar77615	Aam39164	Aaw9093	Aaw9093	Abb74904	Abb74902	Aaw90934	Abb7490	Aaw90936	Abb7494
ΩI	AAB47058	AA018876	AAM41145	AAY24372	AAY24371	AAM39359	AAU74296	ADE28427	AAB36210	AAY96302	AAW88464	AAW48650	AAR77610	AAR66316	ABU08022	AAR77615	AAM39164	AAW90935	AAW90933	ABB74904	ABB74902	AAW90934	ABB74903	AAW90936	ABB74945
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Length	150	150	535	146	146	528	470	471	467	219	476	652	249	117	476	249	120	470	470	470	470	470	470	470	470
% Query Match	100.0	100.0	81.9	79.6	79.4	78.3	74.9	73.7	71.5	69.2	68.4	68.0	68.0	67.9	67.5	66.8	9.99	9.99	9.99	9.99	9.99	66.5	66.5	66.4	66.4
Score		788	45.	27.	625.5	617	σı	80.	563.5	45.	539	536		m	m	526.5	3	3	3	3	2	2	a	3	N
Result No.	н	61	m	4	Ŋ	φ	7	ω	σ	10	11	12	13	14	15	16	17	18	19	70	21	22	23	24	25

Example 5; Fig 6; 55pp; English.

Aab36215 Human imm Aaw83037 Anti-Fas Aab14779 Humanised Aaw9029 Humanised Abb74944 Humanised Abb74998 Humanised Abb43131 Human ova Aar24442 Sequence Aam52162 Humanised Aam52164 Humanised Aam52164 Humanised Aam52165 Humanised Aam52165 Humanised Aam52165 Humanised Aam52166 Humanised Aam52166 Humanised Aam52166 Humanised Aam52166 Humanised Aam52166 Humanised Aam52167 Humanised Aam52167 Humanised	am52158 Humanise am52157 Humanise am52156 Humanise
AAB36215 AAR83037 AAR83037 AAB3037 AAB3037 AB574994 AB574998 AAR52162 AAM52164 AAM52164 AAM52165 AAM52165 AAM52166 AAM52166 AAM52166 AAM52166 AAM52166 AAM52166	AAM52158 AAM52157 AAM52156
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244444444 8	730
	6666 6767 6888 8888
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ALIGNMENTS

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Monoclonal antibody, variable region, heavy chain, light chain, VH; VL; complementarity determining region; CDR; MAb; BO2C11; conformational epitope, factor VIII; KRIX1, von Willebrand factor; hemostasis; intravascular coagulation; arterial thrombosis; arterial restenosis; venous thrombosis; arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel cell lines for producing monoclonal antibodies that bind to factor involved in hemostasis and coagulation cascade, useful for treating and preventing coagulation disorders.
                                                                                      Heavy chain variable region VH of BO2C11.
                                                                                                                                                                                                    Location/Qualifiers
                    AAB47058 standard; protein; 150 AA.
                                                                                                                                                                                                               44. .53
/label= CDR1
68. .86
/label= CDR2
115. .125
/label= CDR3
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                                                                                                                                                                                                                                                                                                                                                            99GB-00016450.
99US-0143891P.
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                                                                (first entry)
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N-PSDB; AAC85451.
                                                                                                                                                                                                                                                                                           WO200104269-A1.
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14-JUL-1999;
                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                 18-JAN-2001.
                                                                08-MAY-2001
                                           AAB47058;
                                                                                                                                                                                                    Key
Domain
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RESULT 1
AAB47058
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This sequence represents the heavy chain variable region of the human monoclonal antibody (MAD), BO2C11. BO2C11 is a human MAD which recognises conformational epitope within the carboxy-terminal of the factor VIII light chains. The MAD produced by the call line of the invention, VIII light chains. The MAD produced by the call line of the invention, KRIXI, specifically recognises the wild type factor VIII ight chain. KRIXI, specifically recognises the wild type factor VIII to von Willebrand factor in a dose dependant manner. The new cell line KRIXI, is deposited with the Belgian Coordinated Collections of Micro-organisms, under a crossion number LMBP 5089CB. KRIXI, or fragments of it, optionally with a thrombolytic agent, are useful for the treament and/or prevention of hemostasis, coaqulation disorder or thrombolic pathologic condition such as intravascular coaqulation, arterial thrombosis, arterial restenois; venous thrombosis or arteriosclerosis, and attenuation of coaqulation in a mammal. An effective and safe antithrombotic therapy is provided which reduces the risk of bleeding in mammals, more particularly in humans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GKGLEWVGSFDPESGESIYAREFQGSVTMTADISTDIAYMELSSLRSDDTAVYYCAVPDP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 788; DB 4; Length 150; 100.0%; Pred. No. 8.1e-61; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 DAFDIWGOGTMVTVSSASTKGPSVFPLGSR 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DAFDIWGQGTMVTVSSASTKGPSVFPLGSR 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human B02C11 heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA018876 standard; protein; 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (COLL-) COLLEN RES FOUND VZW D.
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/label= CDR1
68. .86
/label= CDR2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-JAN-2001; 2001US-0261405P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-JAN-2002; 2002EP-00447005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    115. .125
/label= CD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 150; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 150 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jacquemin MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EP1222929-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA018876;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Region
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The present invention relates to a pharmaceutical composition for the prevention and/or treatment of systemic inflammatory response syndrome (SIRS), sepsie, septic shock, thrombus formation in the microvasculature and disseminated intravascular coagulation in mammals, comprising as an active ingredient a partial inhibitor of factor VIII, in admixture with a carrier. Such inhibitors may include the antibodies B02CII and KRIXI. The present sequence is the heavy chain variable region of B02CII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GKGLEWVGSFDPESGESIYAREFQGSVTWTADTSTDIAYMELSSLRSDDTAVYYCAVPDP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, nootropic, immunosuppressant, cytostatic, gene therapy, cancer, peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MDWIWRILFLVAAATGIHAQVQLVQSGAEVKKPGASVKVSCKVSGYILTELPVHWVGQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP
                                        Pharmaceutical composition for treating systemic inflammatory responseyndrome, sepsis, septic shock and/or thrombus formation in microvasculature in mammals, comprises a partial inhibitor of factor VIII.
                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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0
                                                                                                                                                                                                                                                                                                                                                             Length 150;
                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 788; DB 5;
100.0%; Pred. No. 8.1e-61;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DAFDIWGOGTMVTVSSASTKGPSVFPLGSR 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DAFDIWGQGTMVTVSSASTKGPSVFPLGSR 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ā
                                                                                                                                             Disclosure; Fig 10; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human polypeptide SEQ ID NO 6076.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM41145 standard; protein; 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-00598042.
2000US-00620312.
2000US-0063450.
2000US-00662191.
2000US-00693036.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-00488725.
2000US-00552317.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-DEC-2000; 2000WO-US034263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-00471275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
WPI; 2002-610270/66.
N-PSDB; AAL49254.
                                                                                                                                                                                                                                                                                                                                                Query Match
Tocal Similarity
                                                                                                                                                                                                                                                                                                                             Sequence 150 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200153312-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JAN-2000; 25-APR-2000; 20-JUN-2000; 219-JUL-2000; 203-AUG-2000; 214-SEP-2000; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-OCT-2000;
29-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                 Sest Local Simi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-DEC-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM41145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
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Mon Apr

Wang D; Zhao QA;

Ren F, Wa Zhang J,

Qian XB, Yang Y,

Ma Y, Xue AJ,

HYSE-) HYSEQ INC

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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic acitvity. The polymuclectides are useful in gene therapy. A composition containing a polypeptide or polymuclectide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous solutions of peripheral nervous system diseases, such as latherner's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, activity, chemotextic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GKGLEWVGSFDPESGESIYAREFOGSVTMTADTSTDIAYMELSSLRSDDTAVYYCAVPDP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75 GKGLEWMGAFDPEDGETIYAQKFQGRVIMTEDTSTDTAXMELSSLRSEDTAVYYCATDHG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP 60
                                                                                                                                                               nucleic acids and polypeptides, useful for treating disorders such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 MDCTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; monoclonal antibody; connective tissue growth factor; CTGF; cell proliferation disorder; fibrosis; liver dirhosis; nephritis; skin ulcer; keloid; rheumatoid arthritis; hepatitis; cancer; rheumatic vascular inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
81.9%; Score 645.5; DB 4; Length 535;
Best Local Similarity 84.5%; Pred. No. 8.2e-48;
Matches 125; Conservative 8; Mismatches 14; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         monoclonal antibody against CTGF SEQ ID NO:12
                                                                                                                                                                                                                         Example 2; SEQ ID NO 6076; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D-AFDIWGOGTMVTVSSASTKGPSVFPL 147
                                 Liu C, Asundi V, Chen R,
Wang Z, Wehrman T, Xu C,
Goodrich R, Drmanac RT;
                                                                                                                                                                                     as central nervous system injuries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY24372 standard; protein; 146 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98WO-JP005697
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                                                                                                           2001-442253/47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 535 AA;
                                                                                                                               N-PSDB; AAI60301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9933878-A1
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                                   Tang YT,
Wang J,
Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121
                                                                                                                                                                 Novel
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AAX90020 to AAX90029 encode monoclonal antibodies which react with human connective tissue growth factor (CTGP). AAX24369 to AAX24378 represent these monoclonal antibodies. The antibodies are useful in the diagnosis, prevention and treatment of cell proliferation disorders in which CTGP is implicated, including fibrosis of lung, kidney, liver and other tissues; liver cirrhosis; nephritis; skin ulcers and kelold; rheumatoid arthritis; rheumatic vascular inflammation; hepatitis; and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GKGLEWVGSFDPESGESIYAREFQGSVTMTADISTDIAYMELSSLRSDDTAVYYCA---V 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP
                                                                                                                                                                                                                                                                                                                                                                                                                  1 MDCTWRIFFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGXTLTELSMHWVRQAP
                                                                                                                       New monoclonal antibody reactive with connective tissue growth factor useful in the treatment of cell proliferation disorders.
                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, monoclonal antibody, connective tissue growth factor, CTGF, cell proliferation disorder, fibrosis; liver cirrhosis; nephritis; skin ulcer, keloid, rheumatoid arthritis; hepatitis; cancer; rheumatic vascular inflammation.
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9
                                                                                                                                                                                                                                                                                                                                           Length 146;
                                                                                                                                                                                                                                                                                                                                                                       13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human monoclonal antibody against CTGF SEQ ID NO:10.
                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Takigawa M;
                                                     Takigawa M;
                                                                                                                                                                                                                                                                                                                                           79.6%; Score 627.5; DB 2
84.2%; Pred. No. 7.1e-47;
iive 7; Mismatches 13
                                                                                                                                                                     Claim 17; Page 184-185; 212pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 VTPWYFDYWGOGTLVTVSSASTKGPS 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118 PDPDAPDIWGQGTMVTVSSASTKGPS 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sakamoto S,
                                                       Sakamoto S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY24371 standard, protein; 146
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98JP-00356183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (NISB ) JAPAN TOBACCO INC
                          (NISB ) JAPAN TOBACCO INC
                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tezuka K,
                                                       Tezuka K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-430232/36.
N-PSDB; AAX90022.
                                                                                  WPI; 1999-430232/36.
                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                N-PSDB; AAX90023
                                                                                                                                                                                                                                                                                                                 Sequence 146 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-DEC-1997;
15-DEC-1998;
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15-DEC-1998;
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                                                       Tamatani T,
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Matches 123;
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                                                                                                                                                                         AAX90020 to AAX90029 encode monoclonal antibodies which react with human connective tissue growth factor (CTGF). AAX43459 to AAX4378 represent these monoclonal antibodies. The antibodies are useful in the diagnosis, prevention and treatment of cell proliferation disorders in which CTGF is implicated, including fibrosis of lung, kidney, liver and other tissues; liver cirrhosis; nephritis; skin ulcers and keloid; rheumatoid arthritis; rheumatic vascular inflammation; hepatitis; and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GKGLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYYCA---V 117
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, Zhao (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP
                             New monoclonal antibody reactive with connective tissue growth factor useful in the treatment of cell proliferation disorders.
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Zhang J,
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Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79.4%; Score 625.5; DB 2; 84.2%; Pred. No. 1.1e-46;
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7; Mismatches 13;
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Wehrman T, Xu C, Xue AJ,
R, Drmanac RT;
                                                                                                                     Claim 17; Page 180-181; 212pp; Japanese.
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21-JAN-2000; 2000US-00488725.
25-APR-2000; 2000US-00552317.
20-JUN-2000; 2000US-00598042.
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03-AUG-2000; 2000US-00653450.
14-SEP-2000; 2000US-00653191.
19-OCT-2000; 2000US-00693036.
29-NOV-2000; 2000US-00727344.
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Matches 123; Conservative
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Wang Z, Wehr
Goodrich R,
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                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 146 AA;
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The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nocuropic. Immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous siptem; peripheral nervous system, such as peripheral nervous siptemies, peripheral nervous localised neuropathies and canral nervous system diseases, such as Alzheimer's Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, archerities and thromobylic activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form
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                                                                                                                                                                                                          Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries.
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WPI; 2001-442253/47.
N-PSDB; AAIS8515.
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RESULT 9
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                                                                                                                                                                                                                                                                                  The invention relates to a novel human antibody (I), preferably a human monoclonal antibody which binds to an activation inducible lymphocyte immunomodulatory molecule (AILIM). (I) is useful for modulating signal transduction into a cell mediated by AILIM, for modulating proliferation of AILIM-expressing cells, and for inducing antibody-dependent cytotoxicity against AILIM-expressing cells and/or immune cytolysis or apoptosis of AILIM-expressing cells and/or immune cytolysis or apoptosis of AILIM-expressing cells and/or immune cytolysis or apoptosis of AILIM-expressing cells and/or immune cytolysis or apoptosis of AILIM-expressing cells and/or immune cytolysis or apoptosis of AILIM-expressing cells and/or immune cytolysis or apoptosis of AILIM-expressing cells and/or immune cytolysis or apoptosis of AILIM-expressing cells and/or immune cytolysis or apoptosis of AILIM-expressing cells and/or immune cytolysis or apoptosis of Inflammatory and Contact in the supersession, preventing or prophylaxis of delayed type allergy. (I) is useful for treating and preventing and contact type dermatitis, chronic inflammatory dermatosis, allergic contact-type dermatitis, chronic inflammatory dermatosis, allergic contact-type dermatitis, chronic inflammatory dermatosis, postiasis, autoimmune or allergic disorders, inflammatory dermatosis, postiasis, autoimmune or allergic disorders, inflammatory dermatosis, postiasis, autoimmune or allergic disorders, inflammatory dermatosis, postiasis, autoimmune or allergic disorders, inflammatory dermatosis, postiasis, autoimmune or allergic disorders, inflammatory dermatosis, postiasis, autoimmune or allergic disorders, inflammatory caused by abnormal intestinal immunity, specifically inflammatory intestinal disorders such as ulcerative colitis, pneumonia, hepatitis, nephritis, vasculitis, and pancreatitie. (I) induces no serious antigenicity (HAMA) in a host. AAUV43301 represent anti-human anti-mouse antigenicity to human, i.e., human anti-human anti-human anti-human anti-human anti-human an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial; immunostimulant; anti-HIV; hyperproliferative; cancer; viral; bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy; human; variable region heavy chain; 21-2-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP
                                                                                                                                                                               New human monoclonal antibody that binds to activation inducible lymphocyte immunomodulatory molecule, useful for treating rheumatoid arthritis, multiple sclerosis and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human anti-CD40 antibody 21-2-1 variable region heavy chain protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74.9%; Score 590; DB 5; Length 470; 75.5%; Pred. No. 4.7e-43; Live 8; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----DPDAFDIWGQGTMVTVSSASTKGPSVFPL 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 YDSSGYYHDAFDIWGQCTMVTVSSASTKGPSVFPL 155
                                                                                                                                                                                                                                                         Claim 30; Page 264-266; 300pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADE28427 standard; protein; 471 AA.
18-MAY-2000; 2000JP-00147116
30-MAR-2001; 2001JP-00099508
                                                                                           Hori N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-JAN-2004 (first entry)
                                                      (NISB ) JAPAN TOBACCO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 75.5
Matches 117; Conservative
                                                                                         Tezuka K,
                                                                                                                            WPI; 2002-075313/10
                                                                                                                                               N-PSDB; AAS99472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 470 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADE28427;
                                                                                       Tsuji T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
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The invention relates to a novel chimeric or human monoclonal antibody or its antigen-binding portion that specifically binds to and activates human CB40. The anti-CD40 antibody of the invention demonstrates cytostatic, virucide, antibacterial, immunostimulant and anti-HIV activities and may be useful for treating a hyperproliferative disorder combined immunodeficiency conditions including neutropenia or HIV infection. The anti-CD40 antibodies may also be useful for detecting CD40 in a biological sample in vitro or in vivo, as well as during gene therapy procedures. The current sequence is that of the human anti-CD40 antibody variable region heavy chain protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New chimeric or human monoclonal antibody or its antigen-binding portion that specifically binds to and activates human CD40, useful for enhancing an immune response in a human, or treating cancer, HIV, neutropenia or viral infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GKGLEWVGSFDPESGESIYAREFQGSVTWTADTSTDIAYMELSSLRSDDTAVYYCAVPDP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GQGLEWMGWINPDSGGTNYAQKFQGRVTMTRDTSISTAYWELNRLRSDDTAVYYCARDQP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTBLPVHWVGQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MDWTWRILELVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; immune system associated protein; HISAP-8; immune disorder; infection; autoimmune disease; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  Jia X, Feng X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73.7%; Score 580.5; DB 7; 72.4%; Pred. No. 3.2e-42; ive 11; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----DAFDIWGOGTMVTVSSASTKGPSVFPL 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 LGYCTNGVCSYFDYWGQGTLVTVSSASTKGPSVFPL 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human immune system associated protein HISAP-8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 34; 177pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Corvalan J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB36210 standard; protein; 467
                                                                                                                                                                                                 08-NOV-2002; 2002WO-US036107.
                                                                                                                                                                                                                                                              09-NOV-2001; 2001US-0348980P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 72.49
Matches 113; Conservative
                                                                                                                                                                                                                                                                                                                              (PFIZ ) PFIZER PROD INC. (ABGE-) ABGENIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Bedian V, Gladue RF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-441521/41.
N-PSDB; ADE28426.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 471 AA;
                                                                WO2003040170-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US6135941-A.
                                                                                                                                15-MAY-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB36210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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us-10-044-569b-2.rag

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The present sequence is the human immunoglobulin superfamily protein IGFAM-14. Its gene was isolated from a cDNA library of gallbladder tissue. It is expressed in reproductive, gastrointestinal and cardiovascular tissue, where cancer and inflammation are common. The gene, protein, its antibodies, agonists and antagonists are suitable for disposing and treating many diseases, including cancer, immune system disposing and treating many diseases, including cancer, immune system arteriosclerosis, athma, atherosclerosis, cholecystitis, crown's disease, diabetes mellitus, emphysem, Graves' disease, hepatitis, systemic lupus erythematosus and ulcerative colitis), complications of cancer, haemodialaysis and extracorporeal circulation, trauma and haematopoletic cancer (such as leukemia) and infections caused by bacteria, viruses, fungi or parasites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GKGLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYYCA---- 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunoglobulin superfamily proteins, the agonist and antagonist of the protein is useful for preventing and treating disorders associated with altered levels of the protein such as cancer, immune system disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antigen binding fragment.485; monoclonal antibody; cancer; neoplasm; diagnosis; therapy; melanoma; neuroblastoma; glioma; sarcoma; lung carcinoma; metastasis; anti-idiotype antibody; GD2 antigen; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MDWTWRILFLVAAVTGVGSQVQLVQSGAEVRKPGASVKVSCKASGYTFSDHYIHWVRQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MDWTWRILFLVAAAIGTHAQVQLVQSGABVKKPGASVKVSCKVSGYTLTELPVHWVGQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                               Gorgone GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Monoclonal antibody 4B5 heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69.2%; Score 545.5; DB 3;
69.7%; Pred. No. 1.5e-39;
ive 13; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 SSPVGDAFDIWGQGTWVTVSSASPTSPKVFPL 152
                                                                                                                                                                                                                                                                                                                                           Guegler KJ,
Yang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117 -VPDPDAFDIWGQGTMVTVSSASTKGPSVFPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 88-89; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW88464 standard; protein; 476
                                                                                                                                                 98US-00195853.
98US-0113635P.
99US-0128194P.
                                                                                           99WO-US027566
                                                                                                                                                                                                                                                                                                                                               ξ,Ϋ́
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 106, Conservative
                                                                                                                                                                                                                                                                                                                                               Tang YT, Corley
Lal P, Hillman
                                                                                                                                                                                                                                                                                  (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-387796/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAA27394.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 219 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                       19-NOV-1999;
                                                                                                                                                                                   22-DEC-1998;
07-APR-1999;
                                                                                                                                                        19-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-MAY-1999
                              25-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW88464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                Lu DAM,
                                                                                                                                                                                                                                                                                                                                           Yue H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW88464

1D AAW88

XX AAW8

XX AAW8

DT 10-MA

XX MONOC

XX AATIG

XW AATIG

XW AATIG

XW IUNG

XX HOMO

XX IUNG
SXCCCCCCCCCX BX FFFF XX BXX FFF XX XX FFF X                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention provides the coding and protein sequences for a number of human immune system associated proteins (HISAPs). These can be used in the diagnosis and treatment of various autoimmune disorders, infections and cell proliferation diseases. The diseases include AIDS, adult respiratory distress syndrome, anaemia, asthma, atherosclerosis, crothn's disease, irritable bowel syndrome, multiple sclerosis, myasthenia gravis, osteoarthritis, theumatoid arthritis, scleroderma, systemic lupus erythematosus, arteriosclerosis, cirrhosis and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New human immune system associated proteins (HISAP) and polynucleotides encoding the HISAP, useful for diagnosing, treating or preventing immune or cell proliferative disorders or infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MDCTWRILFLVAAAIGTHAQVQLVQSGAEVKKPGASVQVSCTVSGFTLSDLSVHWVRQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GKGLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYYCAVPDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; immunoglobulin; IGFAM-14; IGFAM; immune disorder; cancer; infection; inflammation; haematopoiesis; AIDS; allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ξ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71.5%; Score 563.5; DB 4; Length 467; 73.0%; Pred. No. 9.5e-41; ive 19; Mismatches 20; Indels 1
                                                                                                                                                                                                                                                                                  Baughn MR;
                                                                                                                                                                                                                                                                                  Guegler KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DFFFDFWGQGTMVTVSSASTKGPSVFPL 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 D-AFDIWGQGTMVTVSSASTKGPSVFPL 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .19
/label= signal_peptide
                                                                                                                                                                                                                                                                                  Corley NC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20. .219
/label= IGFAM-14
34. .117
/label= Ig_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Col 61-64; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY96302 standard; protein; 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human IGFAM-14 immunoglobulin.
                                                                                           98US-00049672.
                                                                                                                                                        98US-00049672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best_Local Similarity 73.0 Matches 108; Conservative
                                                                                                                                                                                                                                                                              Yue H, Lal P,
                                                                                                                                                                                                                 (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-030926/04.
N-PSDB; AAC66526.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 467 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200029583-A2
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                                                                                           27-MAR-1998;
                                                                                                                                                        27-MAR-1998;
                                                                                                                                                                                                                                                                           Tang YT, Yu
Hillman JL,
                              24-OCT-2000
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Query Match

121

AAY96302;

Peptide Protein Domain

EX TYPE FIRE SON X WAY BY THE FIRE SON X WAY

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Baughn MR;

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The present sequence represents a fusion protein comprising of TNF alpha fused to the C-terminus of the heavy chain of the human monoclonal antibody 425 (hmbA25). The hmAb425 has specificity for the human EGF receptor. The invention claims for a new pMCLDHAP tricistronic vector (AAV18036) for the expression of an antibody-cycokine fusion protein, hmAb422-TNF alpha. The TNF alpha sequence can be substituted by the IL-2 sequence. The vector alpo contains a strong promoter/enhancer unit, a selection marker gene and at least two policyirus derived internal ribosomal entry site (IRES) sequences. The vector can be expressed in ammanian host cells for the production of heteromeric fusion proteins. This expression system is claimed to produce the heteromeric proteins in high yields
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oligo:cietronic expression vector - useful for production of, e.g. MAb425/TNF-~a or MAb425/IL-2 antibody fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Von Hoegen I, Burge C, Bruemmer W, Dunker R, Rieke E,
Hauser H, Mielke C;
                                                                                                  Antibody-cytokine fusion protein; tricistronic vecto
TNF alpha; IL-2; IRES; internal ribosome entry site.
                                                          Heavy chain of hmAb425 fused to TNF alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 15; 89pp; English
                    04-AUG-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MERE ) MERCK PATENT GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-207400/18.
N-PSDB; AAV18096.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 652 AA;
                                                                                                                                                              Synthetic.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-SEP-1996;
30-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                        02-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                       WO9811241-A1
                                                                                                                                                                                                                                                                                                                                                                                                  19-MAR-1998
                                                                                                                                                                                                                               Key
Region
                                                                                                                                                                                                                                                                                             Region
This polypeptide comprises the heavy chain variable region of the recombinant human monoclonal antibody (MAb) 4BS. 4BS recognises care recombinant human monoclonal antibody (MAb) 4BS. 4BS recognises care antibodies specific for GD2 antigen antibodies specific for GD2 antigen antibodies specific for GD2 antibodies specific for GD2 antibodies specific for GD2 caredoma, colon adenocarcinoma, amall call lump carcinoma, oncon adenocarcinoma and adenocarcinoma. The invention encompasses 4BS derivatives with immunologic specificity for antibodies specific for GD2. These careforms of antibodies specific for GD2. These careforms of the ABS of the AWBS465). Polyucleotide fragments, comprise regions of the 4BS CVD3 innction and regions spanning the 4BS CDRs. Other derivatives include Fab, F(ab) 2, Fab, scrv and isolated heavy and light chains (see also VDJ junction and regions are also provided, and therapeutic plasmids and correcters, including vaccinia virus vectors, comprising these custing vectoria virus vectors, comprising these custing a host immune response to cancer. Products of the invention can be used in the detection and treatment of e.g. astrocytoma, collaponatoralloma, medulobascoma, prinktive neural collaponatoral vectorarcinoma, medulobascoma, prinktive neural collaponatorarcinoma, entitledial adenocarcinoma, small and collaponatorarcinoma, breast tumours such as ductal and lobular adenocarcinoma, breast tumours such as ductal and lobular denocarcinoma, breast tumours such as ductal and lobular adenocarcinoma, breast tumours such as ductal and lobular cut transitional squamous cell carcinoma of the bladder. B and T cell cynthoma malignant melanoma, soft tissue sarcoma and letomorarcinoma and 
                                                                                                                                                                                                                                                                                                                 New antibody 4B5 polynucleotides and polypeptides - used to develop products for the diagnosis and treatment of cancers and for prophylactic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26; Indels. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68.4%; Score 539; DB 2;
66.9%; Pred. No. 1.3e-38;
iive 16; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                         therapy to reduce risk of recurrence.
                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 79-80; 83pp; English.
                                                                                                                                                                     (NOVO-) NOVOPHARM BIOTECH INC
                                                                                    98WO-IB001046.
                                                                                                                          97US-0051945P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 66.99
Matches 105; Conservative
                                                                                                                                                                                                                                                   WPI; 1999-120769/10.
N-PSDB; AAX06951.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 476 AA;
  WO9902545-A2
                                                                                                                            08-JUL-1997;
                                                                                    08-JUL-1998;
                                          21-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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Welge T;

494 /note= "Heavy chain of human mAb 425"

/note= "TNF alpha"

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97WO-EP004765. 96EP-00114820. 96EP-00115635.

Location/Qualifiers

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68.0%; Score 536; DB 2;
60.6%; Pred. No. 3.4e-38;
ive 14; Mismatches 27;
 Query Match
Best Local Similarity 60.6%
Matches 106; Conservative
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                    9
                                       1 MDWIWRVLFLVAAATSARSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSFDLNWVRQAP
                                                                              61 GKGLEWVGSFDPESGESIXAREFOGSVTMTADTSTDIAYMELSSLRSDDTAVYYC----
                    1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP
                                                                                                                                                            116 ----AVPDPDAFDIWGQGTMVTVSSASTKGPSVFPL 147
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61 GKGLEWVGSFDPESGESIYAREFQGSVTMTADISTDIAYMELSSLRSDDTAVYYCAVPDP 120 9 9 1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP Gaps D----AFDIWGOGTMVTVSS-----ASTKGPSVFPL 147 28; 27; Indels

Length 652;

RESULT 13 AAR77610

AAW48650 standard; protein; 652 AA.

RESULT 12
AAW48650
ID AAW48
XX
AC AAW48

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AAW48650;

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121 GSSPNWYFDVWGQGTLVTVSSASTKGPSVFPL 152
                                                    AAR66316 standard; protein; 117
                                                                                                                                                                                                                                    93WO-JP000603.
                                                                                                                                                                                                                                                        93WO-JP000603
                                                                                                     (first entry)
                                                                                                                                                                                                                                                                         (NISB ) JAPAN TOBACCO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                            (revised)
                                                                                                                                                                                                                                                                                             Matsuda F;
                                                                                                                                                                                                                                                                                                                 WPI; 1995-006791/01.
N-PSDB; AAQ78962.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 117 AA;
                                                                                                                                                                                                                                                                                                                                              DNA fragment c
production of
                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                   10-MAY-1993;
                                                                                                                                                                                                                                                        10-MAY-1993;
                                                                                                                                                                                            WO9426895-A1
                                                                                          25-MAR-2003
03-AUG-1995
                                                                                                                                                                                                                24-NOV-1994.
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Matches 102;
                                                                        AAR66316;
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                                          AAR66316
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Treating glomerulonephritis with antibody against complement C5 component - to inhibit complement induced cell lysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A humanised CDR-grafted and framework sequence-altered Fd, 5G1.1 VH + 16HRL (AAR7761D), includes CDRs derived from mouse anti-C5 monoclonal antibody 5G1.1. It can be co-expressed with a humanised light chain (AAR77612) in human 293 EBNA cells using encoding DNAs subcloned into vector APEX-3P (AAT08476). Such humanised recombinant antibodies retain the ability of MAD 5G1.1 to block human complement C5s generation and thus to reduce glomerular inflammation and kidney dysfunction associated with glomerulonephritis. (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GKGLEWVGSFDPESGESIYAREFQGSVTMTADISTDIAYMELSSLRSDDTAVYYCA--- 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.
                                                                                                                                                                                                                                                                                                                                                                          SH, Rollins S, Rother C, Wang Y, Wilkins JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 249;
                                                                                       Complement C5; haemolysis; kidney; glomerulonephritis; monoclonal antibody; antiinflammatory; antibody engineering; humanised antibody; complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68.0%; Score 535.5; DB 2
69.1%; Pred. No. 1.3e-38;
ive 15; Mismatches 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 VPDPD-AFDIWGQGTMVTVSSASTKGPSVFPL 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 11; Page 119-122; 181pp; English.
                                                                                                                                                                                                                                                                                                                                                                          EE, Nye SH
Thomas TC,
                                                                                                                                                                                20. .249 // label= mat_peptide
45. .54 // label= CDR-H1
                                                                                                                                                              . 19
|abel=_sig_peptide
                                                                                                                                                  Location/Qualifiers
AAR77610 standard; protein; 249 AA.
                                                                                                                                                                                                                        69. .79
/label= CDR-H2
                                                                                                                                                                                                                                            118. .130
/label= CDR-H3
                                                                                                                                                                                                                                                                                                                95WO-US005688.
                                                                                                                                                                                                                                                                                                                                                                          Evans MJ, Matis L, Mueller
Springhorn JP, Squinto SP,
                                                                                                                                                                                                                                                                                                                                  94US-00236208
                                                                     Humanised 5G1.1 VH + IGHRL
                                       (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                    (ALEX-) ALEXION PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 69.19
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1995-392923/50.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 249 AA;
                                                                                                                                                                                                                                                                        WO9529697-A1
                                                                                                                                                                                                                                                                                                                01-MAY-1995;
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                                       25-MAR-2003
15-MAR-1996
                                                                                                                                                                                                                                                                                           09-NOV-1995
                                                                                                                               Synthetic
                   AAR77610;
                                                                                                                                                            Peptide
                                                                                                                                                                                Peptide
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Protein sequences (AAR66295-51) are novel human immunoglobulin heavy chain sequences encoded by novel isolated genes. The genes (AAQ78339-7902) ware isolated and cloned from a series of cosmid constructs: V202; V103; V21; Y6; V24; 3-31; M84; M18 and M31; by PCR amplification using primers AAQ78917-38. The genes are subdivided into 5 families of Vh genes. The fragments cover a region of 800 kb. The DNA fragments were isolated from high molecular weight DNA from human placenta. The DNA was separated by gel elecrophoresis and 35-45 kb fractions were collected. The fragments were ligated with TaqI restriction enzyme. The fragments were injugation products were in vitro packed and infected into E. coli 490A. The fragments were hon subcloned by colony Mybridisation. The Vh genes and the DNA fragments encoding them are useful in producing human immunoglobulin in mammallan hosts. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MDWIWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MDCTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GKGLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYYCA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Primer, PCR, amplify, human; immunoglobulin; variable; heavy chain; cosmid; placenta; vector; pJB81; E.coli; mammalian.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 117;
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hosts.
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87.9%; Pred. No. 6.16-39;
ive 6; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          comprising human immunoglobulin Vh human immunoglobulin in mammalian
Human immunoglobulin variable heavy chain #22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 33; Page 61-62; 130pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABU08022
ID ABU08022 standard; protein; 476 AA.
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10-MAY-2003 (first entry)

ABU08022;

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The invention discloses a recombinant antibody comprising a constant region of monoclonal antibody (Mab) 57 linked to a non-Mab 57 variable region. Rabies is an acute, neurological disease caused by infection of the central nervous system with the rabies virus, a member of the Lyssavirus genus of the family Rhabdoviridae. Also disclosed are methods for producing an isolated recombinant antibody by culturing a host cell, containing a recombinant entibody by culturing a host cell, molecule encoding the antibody. And isolating the nucleic acid molecule encoding the antibody versesed and treating an individual exposed to a pathogen by expressed and treating an individual exposed to a pathogen by antibodies are useful for preventing (vaccine) and treating an individual exposed to a pathogen, e.g. rabies infection. They are also useful for the qualitative and quantitative determination of the rabies virus. The sequences presented are the antibody protein fragments, the nucleic acids encoding them or the PCR primers used to construct the recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New recombinant antibody comprising a constant region of Mab 57 linked to a non-Mab 57 variable region, useful for treating an individual exposed to a pathogen, e.g. rabies infection.
                                                                                                                                  Human; antibody; constant region; monoclonal antibody 57; Mab 57; variable region; Rabies; neurological disease; infection; central nervous system; rabies virus; Lyssavirus; Rhabdoviridae; pathogen; vaccine; virucide; heavy chain.
                                                                                                Monoclonal rabies virus antibody heavy chain, clone 57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 38; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYJE-) UNIV JEFFERSON THOMAS
                                                                                                                                                                                                                                                                                                                                                           21-AUG-2002; 2002WO-US026584.
                                                                                                                                                                                                                                                                                                                                                                                                      21-AUG-2001; 2001US-0314023P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hooper DC, Dietzschold B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-278566/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expression vector
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 476 AA;
                                                                                                                                                                                                                                                                            WO2003016501-A2.
                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                      27-FEB-2003
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61 GKGLEWVGSFDPESGESIYAREFQGSVTWTADTSTDIAYMELSSLRSDDTAVYYCAVPDP 120
                                                                                                                                                                                                                                       61 GQGLEWMGGIIPIFGTANYAQRFQGRLTITADESTSTAYMELSSLRSDDTAVYFCARENL 120
                                                                                                                                       1 MDWTWRFLFVVAAATGVQSQVQLVQSGAEVKKPGSSVKVSCKASGGTFNRYTVNWVRQAP 60
                                                                                                        1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP 60
67.5%; Score 532; DB 6; Length 476; 67.5%; Pred. No. 5.38-38; live 13; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                 121 DA------FDIWGQGTMVTVSSASTKGPSVFPL 147
                                                                                                                                                                                                                                                                                                                                                        DNSGTYYYFSGWFDPWGQGTLVTVSSASTKGPSVFPL 157
                        Best Local Similarity 67.5
Matches 105; Conservative
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Search completed: April Job time : 50.4772 secs

Sequence 157, App Sequence 117, App Sequence 117, App Sequence 66, Appl Sequence 36, Appl Sequence 76, Appl Sequence 76, Appl Sequence 76, Appl Sequence 95, Appl Sequence 96, Appl Sequence 96, Appl Sequence 97, Appl Sequence 57, Appl Sequence 58, Appl Sequence 58, Appl Sequence 58, Appl Sequence 58, Appl Sequence 57, Appl Sequence 176, Appl Sequence 10, Appl Sequence 10, Appl Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli

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Sequence 1, Application US/10044569B
Sequence 2, Application US/10044569B
Publication No. US20030175268A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: D. Collen Research Foundation vzw
APPLICANT: Saint-Remy, Jean-Marie R
APPLICANT: Saint-Remy, Jean-Marie R
TITLE OF INVENTION: Method and pharmaceutical composition for preventing
TITLE OF INVENTION: Method and pharmaceutical inflammatory response syndrome FILE REFERENCE: C1968
CURRENT APPLICATION NUMBER: US/10/044,569B
CURRENT FILING DATE: 2002-01-11
PRIOR APPLICATION NUMBER: US 60/261,405
PRADOR FILING DATE: 2001-01-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature
LOCATION: (3437...(375)
COTHER INFORMATION: complementary determining region number three
US-10-044-569B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (130)...(159)
OTHER INFORMATION: complementary determining region number one FEATURE:
NAME/KEY: misc feature
LOCATION: (202)...(258)
OTHER INFORMATION: complementary determining region number two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 788; DB 14; Best Local Similarity 100.0%; Pred. No. 4.5e-63; Matches 150; Conservative 0; Mismatches 0;
4 US-10-384-933-157
4 US-10-216-484-117
5 US-10-264-049-4263
1 US-09-825-012-66
1 US-09-825-012-80
1 US-09-825-012-80
1 US-09-825-012-80
1 US-09-825-012-80
1 US-09-825-012-80
1 US-09-825-012-80
1 US-09-825-012-85
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2 US-10-04-047-3329
1 US-10-05-9825-012-55
2 US-10-389-223A-10
2 US-10-389-223A-1
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SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 150
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ORGANISM: Homo sapiens
FEATURE:
   US-10-044-569B-2
   Sequence 2, Appli
Sequence 12, Appl
Sequence 10, Appl
Sequence 3, Appli
Sequence 3, Appli
Sequence 14, Appl
Sequence 143, Appl
Sequence 143, Appl
Sequence 143, Appl
Sequence 147, Appl
Sequence 147, Appl
Sequence 147, Appl
Sequence 145, Appl
                                                                                               April 5, 2004, 13:42:12; Search time 35.2792 Seconds (without alignments) 1116.513 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                       US-10-044-569B-2
788
1 MDWTWRILFLVAAATGTHAQ........MVTVSSASTKGPSVFPLGSR 150
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/PCOT_NEW_PUB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/NES0_NEW_PUB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

12: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

15: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

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17: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
                   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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US-10-390-986-12
US-09-859-053-28
US-09-747-669-3
US-10-291-703-3
US-10-255-108A-16
US-10-255-108A-16
US-10-255-108A-16
US-10-256-148A-143
US-10-216-484-143
US-10-384-933-147
US-10-384-933-145
US-10-384-933-145
US-10-384-933-145
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Maximum Match 100%
Listing first 45 summaries
                                                                        - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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Length 150; Indels

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sequence 28, Application US/09859053

Patent No. US20020102658A1

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: TSUJ;

TATLE OF INVENTION: US20020102658A1uaki

APPLICANT: TSUJ;

TITLE OF INVENTION: HUWAN WONOCIONAL ANTIBODY AGAINST A

TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND

TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND

TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND

FILE REFERENCE: 06501-07901

CURRENT APPLICATION NUMBER: US/09/859,053

CURRENT APPLICATION NUMBER: US/09/859,063

PRIOR FILING DATE: 2001-03-30

PRIOR FILING DATE: 2001-03-30

PRIOR FILING DATE: 2000-06-18

NUMBER OF SEQ ID NOS: 43

SEQ ID NO 28

LENGHAMAR: FRACESO for Windows Version 4.0

LENGHAMAR: PRACESO FOR WINDOWS NUMBER: NUMBER OF SEQ ID NOS: 43

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                                                                                                                                                                                                                                                                                                                                                                                                                   1 MDCTWRILELVAAATGTHAQVQLVQFGABVKKPGASVKVSCKVSGYTLTELSMHWVRQAP 60
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Best Local Similarity 75.5%; Pred. No. 9.4e-45;
Matches 117; Conservative 8; Mismatches 22; Indels
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                                                                                                                                                                                                                                       Score 625.5; DB 14;
Pred. No. 1.7e-48;
7; Mismatches 13; I
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                                                                                                                                                                                                                                          Query Match
Best Local Similarity 84.2%;
Matches 123; Conservative
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
ERGTH: 146
                                                                                                                   TYPE: PRT
CAGANISM: Homo sapiens
US-10-390-986-10
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US-09-747-669-3
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Sequence 10, Application US/1039086
Publication No. US20030166011A1
GENERAL INFORMATION:
APPLICANT: Japan Tobacco, Inc.
TITLE OF INVENTION: Monoclonal Antibody Against Connective Tissue Growth Factor
TITLE OF INVENTION: and Medicinal Uses Thereof
FILE REFERENCE: J1-009PCT
CURRENT APPLICATION NUMBER: US/10/390,986
CURRENT FILING DATE: 2003-03-17
PRIOR PILING DATE: 2003-03-17
PRIOR APPLICATION NUMBER: JP P1997-367699
PRIOR APPLICATION NUMBER: JP P1997-367699
PRIOR APPLICATION NUMBER: JP P1998-356183
PRIOR FILING DATE: 1998-12-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Japan Tobacco, Inc.

APPLICANT: Japan Tobacco, Inc.

TITLE OF INVENTION: Monoclonal Antibody Against Connective Tissue Growth Factor FILE SEFERENCE: J1-009PCT

FILE REFERENCE: J1-009PCT

CURRENT APPLICATION NUMBER: US/10/390,986

CURRENT FILING DATE: 2003-03-17

PRIOR APPLICATION NUMBER: US/95/82,337

PRIOR APPLICATION NUMBER: US/95/82,337

PRIOR FILING DATE: 1997-12-25

PRIOR FILING DATE: 1997-12-25

PRIOR FILING DATE: 1998-12-15

NUMBER OF SEQ ID NOS: 27

SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                               9
                                                                                                                                                    GKGLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYYCAVPDP 120
                                    60
                                                                                         1 MDWIWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP 60
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                                                                                                                                                                                                                                                                                  121 DAFDIWGQGTMVTVSSASTKGPSVFPLGSR 150
                                                                                                                                                                                                                                                                                                                                   DAFDIWGQGTMVTVSSASTKGPSVFPLGSR 150
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Sequence 12. Application US/10390986
Publication No. US20030166011A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
CAGANISM: Homo sapiens
US-10-390-986-12
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US-10-390-986-10
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LENGTH: 146
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61 GQGLEWMGGIIPIFGTANYAQRFQGRLTITADESTSTAYMELSSLRSDDTAVYFCARENL 120
                                                                                                                                   61 GKGLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYYC---- 115
                                                                                                                                                                                61 GGGLEWMGWANPNSGKTGYAQKFQGRVTMTRNTSIRTAYMELSGLRSEDTAVYFCARNAD 120
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1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP
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Sequence 16, Application US/1025108A
Sequence 16, Application US/1025108A
Sublication No. US20030157112A1
GENERAL INFORMATION:
APPLICANT: HOOFER, Craig
APPLICANT: HOOFER, Craig
TITLE OF INVENTION: Recombinant Antibodies, and Compositions
TITLE OF INVENTION: and Methods for Making Them
FILE TRIENGERS 321-110
CURRENT FILING DATE: 203-04-10
CURRENT FILING DATE: 2001-05-04
FRIOR PRILORATION NUMBER: US 60/204,518
FRIOR PRILORATION NUMBER: US 60/204,518
FRIOR PRILORATION NUMBER: US 60/314,023
FRIOR FILING DATE: 2001-05-16
FRIOR PRING DATE: 2001-05-16
FRIOR PLING DATE: 2001-05-16
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FOR MAKING AND USING THE SAME
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                                                                                                                                                                                                                                                                                                      116 ----AVPDPDAFDIWGQGTMVTVSSASTKGPSVFPL 147
                                                                                                                                                                                                                                                                                                                                                                                  121 NVEMAAIYHYYGMDVWGQGTTVTVSSASTKGPSVFPL 157
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Best Local Similarity 67.5%; Pred. No. 1.5e-39;
Matches 106; Conservative 13; Mismatches 28;
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TITLE OF INVENTION: RECOMBINANT ANTIBODIES AND CONTITLE OF INVENTION: AND METHODS FOR MAKING AND US FILE OF INVENTION: AND METHODS FOR MAKING AND US FILE OF INTENTION: AND METHODS FOR MAKING AND US FILE OF INTENTION OF STATE CONTINUES. US 10/215,108
PRIOR FILING DATE: 2003-06-13
PRIOR FILING DATE: 2003-06-13
PRIOR FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 60/314,023
PRIOR APPLICATION NUMBER: US 60/314,023
PRIOR FILING DATE: 2001-08-21
PRIOR FILING DATE: 2001-08-21
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Publication No. US20040013672A1
GENERAL INFORMATION:
APPLICANT: Dietzschold, Bernhard
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US-10-225-108A-16
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APPLICANT: Baleh, Mansoor
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS, DESIGNATED
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS, DESIGNATED
TITLE OF INVENTION: AND DETECTION OF CANCERS
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TITLE OF INVENTION: AND DETECTION OF CANCERS
FILE REFERENCE: 31608200102
CURRENT APPLICATION NUMBER: US 09/747,669
FRICR FILING DATE: 2000-12-10
FRICR FILING DATE: 2000-12-10
FRICR FILING DATE: 1998-07-07
FRICR FILING DATE: 1998-07-07
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FRICR FILING DATE: 1998-07-07
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                                             APPLICANT: Saleh, Mansoor
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS, DESIGNATED
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS, DESIGNATED
TITLE OF INVENTION: AND DETECTION OF CANCERS
TITLE OF INVENTION: AND DETECTION OF CANCERS
FILE OF INVENTION: AND DETECTION OF CANCERS
FILE OF INVENTION: AND DETECTION OF CANCERS
FILE REFERENCE: 316082001001
CURRENT APPLICATION NUMBER: US/09/747,669
PRIOR APPLICATION NUMBER: US/09/111,286
PRIOR APPLICATION NUMBER: US/09/111,286
PRIOR FILIND DATE: 1998-07-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PRESENCE FOR Windows Version 4.0
SEQ ID NO 3
LENGTH: 476
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66.9%; Pred. No. 3.6e-40;
ive 16; Mismatches 26; Indels 1
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68.4%; Score 539; DB 9;
Best Local Similarity 66.9%; Pred. No. 3.6e-40;
Matches 105; Conservative 16; Mismatches 26
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         APPLICANT: Dan, Michael D.
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Matches 105; Conserv
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LENGTH: 476
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                                                                                                                                                                                                                                                                            1 MDWIWRFLFVVAAAIGVQSQVQLVQSGAEVKKPGSSVKVSCKASGGIFNRYIVNWVRQAP 60
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                                                                                                                                                                         Length 476;
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                                                                                                                                                                       Query Match 67.5%; Score 532; DB 15; Best Local Similarity 67.5%; Pred. No. 1.5e-39; Matches 106; Conservative 13; Mismatches 28;
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PRIOR APPLICATION NUMBER: US 60/204,518
PRIOR FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 24
SOFWRARE: FASLEEQ for Windows Version 4.0
SEQ ID NO 9
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Publication No. US20030103976A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                    ; TYPE: PRT
; ORGANISM: Human
US-10-461-148-9
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61 GKGLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYCA--- 116
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| Publication No. US2003170817A1
| GREERAL INFORMATION:
| APPLICANT: Baruyama, No. US20030170817A1ufusa
| APPLICANT: Baruyama, Hideyuki
| APPLICANT: Makahara, Kacari
| APPLICANT: Tamaki, Ikuko
| TITLE OF INVENTION: Anti-Fas Anti-Fas Anti-Fas Anti-Fas AppliCANT: Tamaki, Ikuko
| TITLE REPERENCE: 980126CIF/HG
| TITLE REPERENCE: 980126CIF/HG
| CURRENT APPLICATION NUMBER: US/09/499,662
| PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: US 099/053,583
| PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-01
| NUMBER OF SEQ ID NOS: 165
| TENCHMAN OF SEQ ID NOS: 165
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US-10-384-933-143
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                                                                             APPLICANT: Haruyama, No. US20030103976Alufusa APPLICANT: Haruyama, Hideyuki APPLICANT: Nakahara, Kaori APPLICANT: Nakahara, Kaori APPLICANT: Tamaki, Ikuko APPLICANT: Takahashi, Tohru TITE OF INVENTION: ANLE-FRA Antibodies FILE REPERENCE: 980126CIP/HG CURRENT APPLICATION: ANLE-FRA ANTIBODIES CURRENT FILING DATE: 2002-09-99 PRIOR APPLICATION NUMBER: US/09/499,662 PRIOR FILING DATE: 2000-02-09 PRIOR FILING DATE: 2000-02-09 PRIOR FILING DATE: 1998-04-01 NUMBER OF SEQ ID NOS: 165 SEQ ID NO 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 VPDPDAFDIWGQGTMVTVSSASTKGPSVFPL 147
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Sequence 147, Application US/10216484 Publication No. US20030103976A1 GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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SPECICANT: SETIZAMA, NO. US20030170817Alufusa
APPLICANT: Haruyama, Hideyuki
APPLICANT: Haruyama, Hideyuki
APPLICANT: Haruyama, Hideyuki
APPLICANT: Tamaki, Ikuko
APPLICANT: Tamaki, Ikuko
APPLICANT: Tamaki, Tohru
APPLICANT: Takahashi, Tohru
TITLE OF INVENITON: Anti-Pas Anti-Pas Anti-Pas
CURRENT APPLICATION NUMBER: US/10/384,933
CURRENT APPLICATION NUMBER: US/09/499,662
PRIOR PILING DATE: 2000-02-09
PRIOR PELING DATE: 2000-02-09
PRIOR PELING DATE: EARLIER PILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 147
LEWITH A 10
                                                                        1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP
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OTHER INFORMATION: chain of humanized anti-Fas antibody
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Best Local Similarity 68.2%; Pred. No. 6.3e-39;
Matches 103; Conservative 14; Mismatches 30; Indels
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APPLICANY: Haruyama, Hideyuki
APPLICANY: Nakabara, Kaori
APPLICANY: Tamaki, Ikuko
APPLICANY: Tamaki, Ikuko
APPLICANY: Tamaki, Tohru
APPLICANY: Takahabahi, Tohru
TILE OF INVENTION: Anti-Fas Antibodies
FILE REFERENCE: 980126CIP/HG
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Publication No. US20030170817A1
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ORGANISM: Artificial Sequence
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US-10-216-484-145
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61 GKGLEWYGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYYCA--- 116
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Fublication No. US20030170817A1

FUBLICATION: GENERAL INFORMATION:
APPLICANT: Baruyama, Hideyuki
APPLICANT: Tamaia, Hideyuki
APPLICANT: Tamaia, Kacri
APPLICANT: Tamaia, Tkuko
APPLICANT: Tamaia, Tohuu
TITLE OF INVENTION: ALTI-Fas Antibodies
FILE REFERENCE: 980126CIP/HG
CURRENT FILING DATE: 2003-02-05
FRIOR PAPLICATION NUMBER: US/10/384,933
CURRENT FILING DATE: 2000-02-05
FRIOR APPLICATION NUMBER: US/09/499,662
FRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/499,662
FRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1998-04-01

NUMBER OF SEQ ID NOS: 165

LENGTH: 470
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 470;
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CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US/09/499,662
PRIOR FILING DATE: 2000-02-09
PRIOR FILING DATE: 1998-04-01
NUMBER: OF SEQ ID NOS: 165
SEQ ID NO 145
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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61 GKGLEWYGSFDPESGESIYAREFQGSVTWTADTSTDIAYMELSSLRSDDTAVYYCA--- 116
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OTHER INFORMATION: Description of Artificial Sequence: Designed
OTHER INFORMATION: heavy chain of humanized anti-Fas antibody
US-10-216-484-157
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                                                                                                                                                                               Sequence 157, Application US/10216484
Publication No US20030103976A1
GENERAL INFORMATION:
APPLICANT: Serizawa, No. US20030103976Alufusa
APPLICANT: Haruyama, Hideyuki
APPLICANT: Haruyama, Hideyuki
APPLICANT: Takahara, Kaori
APPLICANT: Takahashi, Tohru
APPLICANT: Takahashi, Tohru
APPLICANT: Takahashi, Tohru
APPLICANT: Takahashi, Tohru
APPLICANT: Takahashi, Tohru
APPLICANT: Takahashi, Tohru
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APPLICANT: Takahashi, Tohru
APPLICANT: Takahashi, Tohru
APPLICANT: Takahashi, Tohru
FILE OF INVENTION: AND NUMBER: US/09/499,662
PRIOR FILING DATE: 2000-02-09
PRIOR FILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 157
117 VPDPDAFPIWGQGTMVTVSSASTKGPSVFPL 147
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ORGANISM: Artificial Sequence
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US-10-216-484-157
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Sequence 12, Appl
Sequence 10, Appl
Sequence 110, Appl
Sequence 110, Appl
Sequence 13, Appl
Sequence 45, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 28, Appl
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788
1 MDWTWRILFLVAAATGTHAQ.......MVTVSSASTKGPSVFPLGSR 150
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1: /cgn2_6/ptodata/
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Maximum DB seq length: 2000000000
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Perfect score:
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No.
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Sequence 12, Application US/09582337

Sequence 12, Application US/09582337

Patent No. 656818

GENERAL INFORMATION:

TITLE OF INVENTION: Monoclonal Antibody Against Connective Tissue Growth Factor

TITLE OF INVENTION: and Medicinal Uses Thereof

FILE REFERENCE: J1-009PCT

CURRENT APPLICATION NUMBER: US/09/582,337

CURRENT FILING DATE: 1907-12-25

PRIOR FILING DATE: 1997-12-25

PRIOR FILING DATE: 1998-12-15

NUMBER OF SEQ ID NOS: 27

SOFFWARE: Patentin Ver. 2.0

SEQ ID NO 12
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US-095-337-10
Sequence 10, Application US/09582337
Sequence 10, Application US/09582337
Sequence 10, Application US/09582337
GENERAL INFORMATION:
APPLICANT: Japan Tobacco, Inc.
TITLE OF INVENTION: Monoclonal Antibody Against Connective Tissue Growth Factor
TITLE OF INVENTION: and Medicinal Uses Thereof
FILE REFERENCE: JJ-009PCT
CURRENT APPLICATION NUMBER: US/09/582,337
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                 US-07-634-278-19
US-08-477-728-19
US-08-477-728-19
US-08-487-200-19
US-08-303-5688-31
US-08-578-77-19
US-08-578-77-19
US-08-578-77-19
US-08-603-024-18
US-08-603-024-18
US-08-476-1768-14
US-08-127-7218-14
US-08-127-7218-14
US-08-127-7218-14
US-08-127-7218-14
US-08-434-125-63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 VTPWYFDYWGQGTLVTVSSASTKGPS 146
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Matches 123; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 146
TYPE: PRT
CRGANISM: Homo sapiens
US-09-582-337-12
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US-09-582-337-12
    Query Match
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61 GKGLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYYCAVPDP 120
                                                                                                                                                                                                                                                                                                            1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                             Length 467;
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                                                                                                                                                                                          20; Indels
                                                                                                                                                         Query Match 71.5%; Score 563.5; DB 3; Best Local Similarity 73.0%; Pred. No. 1.4e-44; Matches 108; Conservative 19; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 535; DB 3;
Pred. No. 1.3e-42;
                                                                                                                                                                                                                                                                                                                                                                                          121 DFFFDFWGQGTMVTVSSASTKGPSVFPL 148
                                                                                                                                                                                                                                                                                                                                                           121 D-AFDIWGQGTMVTVSSASTKGPSVFPL 147
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TELEX: 200154
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
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87.9%;
             EBNGTH: 467 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; LIBRARY: LUNGTUT11

; CLONE: 2747531

US-09-049-672A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 117 amino acids
amino acid
SEQUENCE CHARACTERISTICS:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                61 GKGLEHMGSFDPEDGETIYAQKRQGRVIMTEDTSTDTAXMELSSLRSEDTAVYCATSTV 120
                                                                                                                                                                                                                                                                                                             1 MDCTWRILFLVAAATGTHAQVQLVQFGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAP 60
                                                                                                                                                                                                                                                                                1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP
                                                                                                                                                                                                                                               Gaps
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APPLICANT: Lal, Preeti
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Au-Young, Janice
APPLICANT: Au-Young, Janice
APPLICANT: Corley, Neil C.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                               3;
                                                                                                                                                                                                             Query Match 79.4%; Score 625.5; DB 4; Length 146; Best Local Similarity 84.2%; Pred. No. 6.4e-51; Matches 123; Conservative 7; Mismatches 13; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTY:

ZIF: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: ISM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
CURRENT FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: JP P1997-367699
PRIOR FILING DATE: 1997-12-25
PRIOR APPLICATION NUMBER: JP P1998-356183
PRIOR FILING DATE: 1998-12-15
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: 146
                                                                                                                                                                                                                                                                                                                                                                                                                                    121 VTPWYFDYWGQGTLVTVSSASTKGPS 146
                                                                                                                                                                                                                                                                                                                                                                                                               118 PDPDAFDIWGQGTMVTVSSASTKGPS 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/09049672A Patent No. 6135941 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Cerrone, Michael (
REGISTRATION NUMBER: 39
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: HEREWITH CLASSIFFCATION: 536 PRIOR APPLICATION DATA: APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         650-845-4166
                                                                                                                                                TYPE: PRT
CRGANISM: Homo sapiens
US-09-582-337-10
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CITY: Palo Alto
STATE: CA
COUNTRY: USA
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US-09-049-672A-8
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61 GKGLEWVGSFDPESGESIYAREFQGSVTMTADISTDIAYMELSSLRSDDTAVYYCAVP-D 119
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,968
FILING DATE: U1-SEP-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 78913/1993
FILING DATE: 11-RR-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGET L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: 25,618
TELEFRANCE/DOCKET NUMBER: EDA=1
TELEFRANCE/OWNICATION INFORMATION:
TELEFRANCE/OWNICATION INFORMATION:
TELEFRANCE: 202-628-5197
TELEFRANCE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-HIV MONOCLONAL ANTIBODY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65.2%; Score 513.5; DB 3 69.3%; Pred. No. 1.5e-40; ive 16; Mismatches 25
                                                              118 PDPDAFDIWGQGTMVTVSSASTKGPSVFPL 147
                                                                                        ; Sequence 38, Application US/08513968
; Patent No. 6114143
                                                                                                                                                                                                                                                                                                                                          APPLICANT: OSATOMI, Kiyoshi
APPLICANT: KIMACHI, Kazuhiko
APPLICANT: HIGUCHI, Hirofumi
APPLICANT: TOXYOSHI, Sachio
TITLE OF INVENTION: ANTI-HIV M
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 PDAFDIWGQGTMVTVSS 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 3 SEQUENCE CHARACTERISTICS: LENGTH: 137 amil
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: protein US-08-513-968-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 95; Conserva'
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APPLICANT:
APPLICANT:
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                                                                             1. MDCTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAP 60
                                                                                                                          61 GKGLEWVGSFDPESGESIYAREFQGSVTWTADTSTDIAYMELSSLRSDDTAVYYCA 116
                                                                                                                                                61 GKGLEWMGGFDPEDGETIYAQKPQGRVTWTEDTSTDTAYWELSSLRSEDTAVYYCA 116
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  0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 236;
                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Tang, Y. Tom
APPLICANT: Yue, Henry
APPLICANT: Au-Young, Janice
APPLICANT: Corley, Nail C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
APPLICANT: Baughn, Mariah R.
APPLICANT: SEQUENCES: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 522.5; DB 3; Length; Pred. No. 4e-41; 16; Mismatches 30; Indels
  8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastESQ for Windows Version 2.0
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                   Sequence 13, Application US/09049672A
Patent No. 6135941
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                 Hillman, Jennifer L.
Lal, Preeti
Tang, Y. Tom
Yue, Henry
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CLASSIFICATION: 536
PRIOR APPLICATION: 536
PRIOR APPLICATION DATE:
PILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: CETTON, MICHAEL C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET WINBER: PF-
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 67.3%;
Matches 101; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 236 amino acids
TYPE: amino acid
STRANDEDNESS: single
102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 650-855-05
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CITY: Palo Alto
STATE: CA
COUNTRY: USA
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; CLONE: 3551457
US-09-049-672A-13
Matches
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61 GKGLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYYCAVPDP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MDWIWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 476;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,939
                             Patent No. 5875961
GENERAL INFORMATION:
APPLICANT: CROWE, JAMES SCOTT
APPLICANT: LEWIS, ALAN PETER
TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
NUMBER OF SEQUENCES: 46
CORRESSED NOTHWELL, FIGG, ERNST & KURZ
STREET: 555 THIRTEENTH ST. N.W.
CITY: MASHINGTON
STATE: D. C.
COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64.0%; Score 504; DB 2;
62.5%; Pred. No. 4.7e-39;
tive 16; Mismatches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION: 435
APPLICATION DATA:
APPLICATION NUMBER: US 07/952640
FTLING DATE: 01-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: ERNGY: BARBARA G
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1808-118
TELEPHONE: (202) 783-6440
TELEPHONE: (202) 783-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
; Sequence 10, Application US/08378939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (202) 783-6031 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    476 amino acids
amino acid
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Best Local Similarity 62.5%
Matches 100; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-378-939-10
                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-301-593-43
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                                                                                                                            APPLICANT: BURKLY, LINDA C.
APPLICANT: CHISHOLM, PATRICIA L.
APPLICANT: THOMAS, DAVID W.
APPLICANT: THOMAS, DAVID W.
APPLICANT: ROSA, MARCARET D.
APPLICANT: ROSA, MARCARET D.
TITLE OF INVENTION: ANTI-CO4 ANTIBODY HOMOLOGS USEFUL IN
TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESSE: ALLEGREFUT F. MITTORIAL CORRESPONDENCE ADDRESSE: ALLEGREFUT F. MITTORIAL CORRESPONDENCE ADDRESSES: ALLEGREFUT F. MITTORIAL CORRESPONDENCE ADDRESSES: ALLEGREFUT F. MITTORIAL CORRESPONDENCE ADDRESSES: ALLEGREFUT F. MITTORIAL CORRESPONDENCE ADDRESSES: ALLEGREFUT F. MITTORIAL CORRESPONDENCE ADDRESSES: ALLEGREFUT F. MITTORIAL CORRESPONDENCE ADDRESSES: ALLEGREFUT F. MITTORIAL CORRESPONDENCE ADDRESSES: ALLEGREFUT F. MITTORIAL CORRESPONDENCE ADDRESSES: ALLEGREFUT F. MITTORIAL CORRESPONDENCE ADDRESSES: ALLEGREFUT F. MITTORIAL CORRESPONDENCE ADDRESSES: ALLEGREFUT F. MITTORIAL CORRESPONDENCE ADDRESSES: ALLEGREFUT F. MITTORIAL CORRESPONDENCE ADDRESSES: ALLEGREFUT F. MITTORIAL CORRESPONDENCE ADDRESSES: ALLEGREFUT F. MITTORIAL CORRESPONDENCE ADDRESSES: ALLEGREFUT F. MITTORIAL CORRESPONDENCE ADDRESSES: ALLEGREFUT F. MITTORIAL CORRESPONDENCE ADDRESSES: ALLEGREFUT F. MITTORIAL CORRESPONDENCE ADDRESSES: ALLEGREFUT F. MITTORIAL CORRESPONDENCE ADDRESSES: ALLEGREFUT F. MITTORIAL CORRESPONDENCE ADDRESSES F. MITTORIAL CORRESPONDENCE ADDRESSES F. MITTORIAL CORRESPONDENCE ADDRESSES F. MITTORIAL CORRESPONDENCE ADDRESSES F. MITTORIAL CORRESPONDENCE ADDRESSES F. MITTORIAL CORRESPONDENCE ADDRESSES F. MITTORIAL CORRESPONDENCE ADDRESSES F. MITTORIAL CORRESPONDENCE ADDRESSES F. MITTORIAL CORRESPONDENCE ADDRESSES F. MITTORIAL CORRESPONDENCE ADDRESSES F. MITTORIAL CORRESPONDENCE ADDRESSES F. MITTORIAL CORRESPONDENCE ADDRESSES F. MITTORIAL CORRESPONDENCE ADDRESSES F. MITTORIAL CORRESPONDENCE ADDRESSES F. MITTORIAL CORRESPONDENCE ADDRESSES F. MITTORIAL CORRESPONDENCE ADDRESSES F. MITTORIAL CORRESPONDENCE ADDRESSES F. MITTORIAL CORRESPONDENCE ADDRESSES F. MITTORIAL CORRESPONDENCE ADDRESSES F. MIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSE:
ADDRESSE:
ADLEGRETTI & WITCOFF, LTD.
STREET: 10 SOUTH WACKER DRIVE
CITY: CHICAGO
STATE: ILLINOIS
COUNTRY: U.S.A.
ZIP: 60606
COMPUTER: ILDINOIS
COMPUTER: REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BEN PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WOND PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O7/916,098A
FILING DATE: UJY 24, 1992
CLASSIFICATION NUMBER: PC-TOS/MS91/08843
FILING DATE: NO. S871732ember 27, 1991
CLASSIFICATION NUMBER: PC-TOS/MS-DOS
CLASSIFICATION NUMBER: PC-TOS/MS-DOS
CLASSIFICATION NUMBER: PC-TOS/MS-DOS
FILING DATE: NO. S871732ember 27, 1990
CLASSIFICATION NUMBER: 26,949
REPERENCE/DOCKET NUMBER: 92,310-G
TELEFHONE: (312) 715-1234
TELEFHONE: (312) 715-1234
TELEFHONE: (312) 715-1234
TELEFAX: 910/221-5317
INFORMATION FOR SED ID NO: 45:
SEQUENCE CHARACTERISTICS:
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                                                                                                                            Sequence 45, Application US/07916098A Patent No. 5871732
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amino acid
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Best Local Similarity 64.5*
Matches 98, Conservative
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61 GQGLEWMGGIIPLFGTPTYSQNFQGRVTITADKSTSTAHMELTSLRSEDTAVYXCAT--- 117
                                                                                                                                                                                                                                                                                                               Sequence 43, Application US/09301593A
Sequence 43, Application US/09301593A
BAPLICANT: Bark, John E.
APPLICANT: Garin-Chesa, Pilar
APPLICANT: Garin-Chesa, Dilvier
APPLICANT: Saldanha, Jose W.
APPLICANT: Saldanha, Jose W.
APPLICANT: Saldanha, Jose W.
APPLICANT: Scaldanha, Jose W.
APPLICANT: Rettig, Wolfgang J.
TITILE OF INVENTION: FAP-specific Antibody with Improved Producibility
FILE REFERENCE: 0652.189001
CURRENT APPLICATION NUMBER: US/09/301,593A
CURRENT FILING DATE: 1999-04-29
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RESULT 8 US-08-378-939-10

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                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 63.8%; Score 503; DB 4; Length 472; Best Local Similarity 63.6%; Pred. No. 5.7e-39; Matches 98; Conservative 15; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:

APPLICANT: Rettleborough, Catherine A.

APPLICANT: Saldanha, Jose
APPLICANT: Saldanha, Jose
APPLICANT: Saldanha, Jose
ATILE OF INVENTION: Humanized and Chimeric Monoclonal
TITLE OF INVENTION: Antibodies
NUMBER OF SEQUENCES: 4

CORRESSEE: Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Boulevard, Suite 1400
CITY: Arlington
STRIET: 2200 Clarendon Boulevard, Suite 1400
CITY: Arlington
STRIET: Virginia
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: PREDETION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP92/00480
FILING DATE: 06-NOV-1992
CLASSIFICATION NUMBER: EP 911933892
FRIUNG APPLICATION DATA:
APPLICATION NUMBER: EP 911933892
FRIUNG APPLICATION DATA:
APPLICATION NUMBER: BP 911933892
FRIUNG APPLICATION DATA:
APPLICATION NUMBER: BP 911933892
FRIUNG APPLICATION NUMBER: BP 911933892
FRIUNG APPLICATION NUMBER: BP 911933892
FRIUNG APPLICATION NUMBER: Merck 1430
FRIESCOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
THE TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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EARLIER APPLICATION NUMBER: BP 98107925.4
EARLIER FILING DATE: 1998-04-30
EARLIER FILING DATE: 1998-05-18
NUMBER OF SEQ ID NOS: 108
SOFTWARE: PALENTIN Ver. 2.0
SEQ ID NO 43
LENGTH: 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 28, Application US/07946421
Patent No. 5558864
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 140 amino acids
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                                                                                                                                                                                                                                                                                TYPE: PRT
CRGANISM: Homo, sapiens
US-09-301-593-43
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US-09-982-337-8

Sequence 8, Application US/09582337

Patent No. 652618

GENERAL INFORMATION:
TITLE OF INVENTION: and Medicinal Uses Thereof

TITLE OF INVENTION: and Medicinal Uses Thereof
TITLE OF INVENTION: and Medicinal Uses Thereof

TITLE OF INVENTION: and Medicinal Uses Thereof

CURRENT APPLICATION NUMBER: US/09/582,337

CURRENT FILING DATE: 2000-06-23

PRIOR APPLICATION NUMBER: UP P1997-367699

PRIOR APPLICATION NUMBER: UP P1998-356183

NUMBER OF SEQ ID NOS: 27

SEQ ID NO 8: 27

SEQ ID NO 9.
                                                                                                                                                                                                                                                                                           61 GKGLEWVGSFDPESGESIYAREFQGSVTMTADISTDIAYMELSSLRSDDTAVYYCAVPDP 120
                                                                                                                                                                                                                                                                                                                        61 GQGLEWVGEFNPSNGRINYNEKFKSRVIMTLDTSTNTAYMELSSLRSEDTAVYYCASRDY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56 WVRQAPGQGLEWMGWINPNSSGTHYAQMFQGRVTVTRDTSISTAYMELSRLKSDDTAVYY 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55 WVGQAPGKGLEWVGSFDPESGESIYAREPQGSVTWTADTSTDIAYMELSSLRSDDTAVYY 114
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                                                                                           Length 140;
                                                                                                                                               26; Indels
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Sequence 102, Application US/08137117D
GENERAL INFORMATION:
APPLICANT: STOCK KAN
APPLICANT: BENDIG, Mary
APPLICANT: BENDIG, Mary
APPLICANT: BENDIG, Mary
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 496; DB 4;
Pred. No. 6.9e-39;
9; Mismatches 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115 CAVPDPDA-----FDIWGQGTMVTVSSASTKGPS 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 CAREGIAAAAIYGMDVWGQGTTVTVSSASTKGPS 149
                                                                                                63.6%; Score 501; DB 1;
68.6%; Pred. No. 2.2e-39;
                                                                                                                                         14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                        121 DYDGRYFDYWGQGTLVTVSS 140
                                                                                                                                                                                                                                                                                                                                                                                           121 D----AFDIWGQGTMVTVSS 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66.9%;
                                                                                             Query Match 63.6% Best Local Similarity 68.6% Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 66.9
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-582-337-8
; TYPE: amino acid
; TOPOLOGY: linear
US-07-946-421-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
US-08-137-117D-102
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3: Foley & Lardner
3000 K Street, N.W., Suite 500
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TELEX: 904136
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
"VPE: amino acid
"TELEX."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 DAFDIWGQGTMVTVSS 136
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120 NRFAYWGQGTLVTVSS 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , MOLECULE TYPE: protein US-08-436-717-102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 93; Conserva
                                                       Washington
   ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62.5%; Score 492.5; DB 1; Length 135; 68.4%; Pred. No. 1.3e-38; ive 16; Mismatches 26; Indels 1
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Patent No. 5817790:
GENERAL INFORMATION:
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: SALO, Mary
APPLICANT: SALO, Mary
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117D
FILNG DATE: C1-DEC 1993
PRIOR APPLICATION NUMBER: US/08/137,117D
FILNG DATE: 24-APR-1992
PRIOR APPLICATION NUMBER: US/08/4
FILING DATE: 24-APR-1992
PRIOR APPLICATION NUMBER: US/08/4
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 3-95476
FILING DATE: 19-FEB-1991
APPLICATION NUMBER: 25,258
FILING DATE: 25-APR-1991
APPLICATION NUMBER: 25,258
REGISTRATION NUMBER: 25,258
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                        , Suite 500
                                                                                                                                                                             CCUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEX: 90416
INFORMATION FOR SEQ ID NO: 102: SEQUENCE CHARACTERISTICS: LENGTH: 135 amino acids TVPE: amino acids
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120 NRFAYWGQGTLVTVSS 135
                                                          3: Foley & Lardner
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Matches 93; Conservative
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                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & L
STREET: 3000 K Stree
NUMBER OF SEQUENCES:
                                                                                                                     Washington
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US-08-436-717-102
                                                                                                               CITY: Walstrand STATE: D
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61 GKGLEWVGSFDPESGESIYAREFQGSVTMTADISTDIAYMELSSLRSDDTAVYYCAVPDP 120
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US-08-649-100-41
US-08-649-100
; Sequence 41, Application US/08649100
; Patent No. 6114507
; GENERAL INFORMATION:
APPLICANT: SHIRAKAWA, KAMON
; APPLICANT: NAGATA, SHIGEKAZU
; APPLICANT: NAGATA, SHIGEKAZU
; APPLICANT: NAGATA, SHIGEKAZU
; APPLICANT: NAGATA, SHIGEKAZU
; TITLE OF INVENTION: ANTI-FAS LIGAND ANTIBODY
; TITLE OF INVENTION: METHOD USING THE ANTI-FAS LIGAND ANTIBODY
; UNDERRO OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7;
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CONDUCTAY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: EMPC compatible

COMPUTER: Floppy disk

COMPUTER: Floppy disk

COMPUTER: EMPC compatible

COMPUTER: EMPC compatible

COMPUTER: EMPC compatible

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/137,117

FILING DATE: 24-APR-1992

APPLICATION NUMBER: US/08/137,117

FILING DATE: 24-APR-1992

APPLICATION NUMBER: US 4-32084

FILING DATE: 19-FEB-1992

APPLICATION NUMBER: US 3-95476

FILING DATE: 25-APR-1091

APPLICATION NUMBER: US 3-95476

FILING DATE: 25-APR-1091

APPLICATION NUMBER: 25-APR-1091

APPLICATION NUMBER: 25-APR-1091

APPLICATION NUMBER: 25-APR-1091

APPLICATION NUMBER: 25-APR-1091

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APPLICATION NUMBER: 25-APR-1091

APPLICATION NUMBER: 25-APR-1091

APPLICATION NUMBER: 25-APR-1091

APPLICATION NUMBER: 25-APR-1091

APPLICATION NUMBER: 25-APR-1091

APPLICATION NUMBER: 25-APR-1092

REFERENCE/DOCKET NUMBER: 25-ABOX

TELECOMMUNICATION INDERN: 25-250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 62.4%; Score 492; DB 3; Length 136; Best Local Similarity 68.4%; Pred. No. 1.5e-38; Matches 93; Conservative 13; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 100, Application US/08137117D
Patent No. 579506
Patent No. 579506
GENERAL INFORMATION:
PAPPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: SATO, Koh
APPLICANT: JONES, Steven
APPLICANT: SALDANHA, USES
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
TITLE OF INVENTION: Lardner
STREEF: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
                                         CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDTUM TYPE: FORM:
MEDTUM TYPE: FORM:
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/NM-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/649,100
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: WURPHY JR, GERALD M
REGISTRATION NUMBER: 28,97
REGISTRATION NUMBER: 28,97
REGISTRATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELEFACOM (703) 205-8050
TELEFAC: (703) 205-8050
TELEFAC: (703) 205-8050
TELEFAC: (703) 205-8050
TELEFACTION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
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ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DC
SOFTWARE: Patentin Pelasen 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 DAFDIWGQGTMVTVSS 136
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amino acid
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April 5, 2004, 13:25:01; Search time 11.533 Seconds (without alignments) 1184.358 Million cell updates/sec
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1 METPAQLLFLILLWLPDTTG.....TRLBIKGTVAAPSVFIFPPS 142
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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519 520 519 520 5113 5113 50 5110 50 508 50 508 50 508		antibody 31-Feb-1 10n: 8481 11,0 m.; 11,0 the ption: N noc numb noc numb noc system i prelit	family: 1/Domain: / Match Local Sir	M WE	61 PC	121 00	a chain - human es: Home sapiens (man) 20-Feb-1995 #sequence_re sion: \$2063! S.K.; Bridges, L.S.; Koog ed to the EMBL Data Librr ence number: \$2063! sipon: \$2063! si preliminary ule type: mRNA ues: 1-145 < LEE> -references: BMBL: 211903; family: immunoglobulin V rds: heterotetramer; imm 1/Domain: immunoglobulin immunoglobulin
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A;Title: Autoantibody-associated kappa light chain variable region
A;Reference number: PL0021; MUID:88171307; PMID:3127527
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C)Superfamily: immunoglobulin V region; immunoglobulin homology
C)Keywords: immunoglobulin
F)36-111/Domain: immunoglobulin homology <IMM>
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Pred. No. 8.5e-42;
4; Mismatches 6; Indels
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Chen, P.P.; Carson, D.A.
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                                                                                                                                                                          A,Accession: PL0021
A,Molecule type: mRNA
A,Residues: 1-129 «KIP>
C,Comment: The protein is one of
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A, Cross-references: GDB.136266
A, Genes of the consists of two identical light (kapp bosition: 2p12-2p11
C, Comp bosition: 2p12-2p11
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C;Species: Homo sapiens (man)
C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 21-Jan-2000
C;Accession: PL0022
B;Kipps, T.J.; Tomhave, E.; Chen, P.P.; Carson, D.A.
J. Exp. Med. 167, 840-852, 1988
A;Title: Autoantibody-associated kappa light chain variable region gene expressed in A;Accession: PL0021; MUID:88171307; PMID:3127527
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C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 21-Jan-2000
C;Accession: PL0021
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Best Local Similarity 93.8%; Pred. No. 1.4e-42;
Matches 120; Conservative 4; Mismatches 4; Indels
                                                                                                                                                14; Indels
                                                             DB 2;
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                                                   Score 627; DB 2,
Pred. No. 9e-43;
9; Mismatches 1
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                                    Query Match
Best Local Similarity 83.81
Warches 119; Conservative
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QGTKVEIK 128
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C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
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Species: Homo sapiens (man)
Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
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PGOAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCOKYGTSAITFG
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C.Species: Homo sapiens (man)
C.Jate: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-200
C.Jaccession: $40327
R.J. Immunol. 23, 3248-3271, 1993
Eur. J. Immunol. 23, 3248-3271, 1993
A.JTile: Expressed human immunoglobulin chi genes and their hypermutation.
A.Reference number: $40312; MUID:94080891; PMID:8258341
A.Status: preliminary; translation not shown
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;36-111/Domain: immunoglobulin homology <IMM>
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Kriee, S.K.; Bridges, L.S.; Koopman, W.J.; Schroeder, H.W. submitted to the EMBL Data Library, April 1992

A;Reference number: S20631

A;Accession: S20636

A;Accession: S20636

A;Accession: Preliminary

A;Acture: preliminary

A;Residues: 1-128 < LEE>
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82.9%; Score 608; DB 2; L.
Best Local Similarity 91.4%; Pred. No. 2.5e-41;
Matches 117; Conservative 4; Mismatches 7;
                                                                                                                                                      142
                                                                                                                                                                                                       120 GGTKVEIKRTVAAPSVFIFPPS 141
                                                                                                                                                      121 OGTRLEIKGTVAAPSVFIFPPS
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Best Local Similarity 94.2%;
Matches 114; Conservative
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C.Species: Homo sapiens (man)
C.Species: 30-Unn-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C.Accession: PLO106
R.Silberstein, L.E.; Litwin, S.; Carmack, C.E.
B.Silberstein, L.E.; Litwin, S.; Carmack, C.E.
A.Title: Red.169, 1631-1643, 1989
A.Title: Relationship of variable region genes expressed by a human B cell lymphoma secr
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A; Molecule type: mRNA
A; Residues: 1-144 «SIL»
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 1-20/Domain: signal sequence #status predicted «SIG»
F; 26-110/Domain: V region «VRE»
F; 36-110/Domain: immunoglobulin homology «IMM»
F; 44-54/Region: complementarity-determining 1
F; 70-76/Region: complementarity-determining 2
F; 109-115/Region: complementarity-determining 3
F; 116-127/Domain: J region «JRG»
F; 128-144/Domain: C region (fragment) «CRE»
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83.0%; Score 608.5; DB.2; Length 144;
Best Local Similarity 85.2%; Pred. No. 2.6e-41;
Matches 121; Conservative 5; Mismatches 15; Indels 1
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Pred. No. 8.8e-42;
4; Mismatches 6; Indels
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Best Local Similarity 92.2%;
Matches 118; Conservative 4
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                                                                     QGTRLEIK 128
            QGTRLEIK
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A;Residues: 1-116 <GRA>
A;Note: this sequence was translated from an aberrantly rearranged kappa gene from lamb
C;Genetics:
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                                                            61 PGQAPRLLISGASRRATGIPDRFSGSGSGTDFTLTISRLEPEDFAMYYCQQYGSTPRTFG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 PRILIYGASTRATGIPDRFSGSGSTDFTLTISRLEPEDFAVYYCQKYGTSAITFGQGTR 124
                              PGQAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQKYGTSAITFG 120
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C;Date: 22-Nov-1993 #sequence_revision 14-Jul-1995 #text_change 21-Jan-2000
C;Accession: S20633
K;Lee, S.K.; Bridges, L.S.; Koopman, W.J.; Schroeder, H.W.
submitted to the EMBL Data Library, April 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 AQLLFLLLUMLPDTTGBIALTQSPGTLSLSPGERATLSCRASQSFSSSYLAWYQQKPGQA
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A;Accession: $20633
A;Accession: $20633
A;Accession: $20633
A;Accession: $20633
A;Accession: $20633
A;Accession: $20633
A;Cossion: preliminary
A;Residues: 1-124 <LEE>
A;Cossion: Light <LEE>
C;Superfamily: immunoglobulin W region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;32-107/Domaîn: immunoglobulin homology <IMM>
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A introns: 17/1
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>F;1-20/Domain: immunoglobulin homology <IVM>
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Best Local Similarity 95.7<sup>3</sup>
Matches 110; Conservative
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C;Date: 31-Dec-1989 #sequence_revision 30-Sep-1991;#text_change 21-Jan-2000
C;Date: 31-Dec-1989 #sequence_revision 30-Sep-1991;#text_change 21-Jan-2000
C;Accession: A32274
R;Newkirk, M.M.; Gram, H.; Heinrich, G.F.; Oestberg, L.; Capra, J.D.; Wasserman, R.L.
J. Clin. Invest. 81, 1511-1518, 1988
A;Title: Complete protein sequences of the variable regions of the cloned heavy and ligh actors of the Wa idiotypic family.
A;Reference number: A92767; MUD:88213701; PMID:2452836
A;Accession: A32274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Cross-references: EMBL:Z11890; NID:g33202; PIDN:CAA77944.1; PID:g33203; EMBL:Z11895; C,Superfanily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin complexity filthomain: immunoglobulin homology c!Keywords: heterotetramer; immunoglobulin homology c!Keywords: nemunoglobulin homology c!MM>
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A.Residues: 1-129 <NEW>
A.Korosa-references: GB.MZ0031
A.Korosa-references: GB.MZ0031
A.Note: the authors translated the codon GAT for residue 17 as Ala
A.Note: this sequence was determined from the differentiated gene
C.Superfamily: immunoglobulin V region; immunoglobulin homology
C.Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-129/Product: Ig kappa chain V-III region EVI-15 #status predicted <KV3>
F:36-111/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                    Grappa chain V region - human C'Species: Homo sapiens (man) C'Species: Homo sapiens (man) C'Species: Homo sapiens (man) C'Species: Homo sapiens (man) C'Species: Homo sapiens (man) C'Species: Homo sapiens S20637; S20632 C'Accession: S20637; S20632 R'Lee, S.K.; Bridges, L.S.; Koopman, W.J.; Schroeder, H.W. Sulfages, L.S.; Koopman, W.J.; Schroeder, H.W. A'Reference number: S20631 A'Reference number: S20637 A'Reference number: S20637 A'Reference number: S20637 A'Residues: Hellinary A'Rolecule type: mRNA A'Rolecule type: RRNA A'Rolecule type: RRNA A'Residues: 1-130 <LEE>
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Pred. No. 5.6e-40;
7; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 594; DB 2; Length 13
Pred. No. 3.2e-40;
4; Mismatches 8; Indels
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Best Local Similarity 89.1%;
Matches 114; Conservative
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Best Local Similarity 89.2%;
Matches 116; Conservative
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1 METPAQLIFILILIMIPDITIGEIVLIQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQK 60
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R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Bur. J. Immunol. 23, 3248-3271, 1999
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40325
A;Status: preliminary; translation not shown
A;Residues: 1-129 <KLE>
A;Residues: 1-129 <KLE>
A;Cross-references: EMBL:X72435; NID:9441338; PIDN:CAA51103.1; PID:9441339
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;35-110/Domain: immunoglobulin homology <IMM>
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77.4%; Score 567.5; DB 2; Length 131;
Best Local Similarity 85.5%; Pred. No. 4e-38;
Matches 112; Conservative 5; Mismatches 13; Indels 1
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PO1617 PO1608 PO1603 PO1601 PP3593 PO1634 PO1665 PO1593 PO1593

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P. SEQUENCE FROM N.A.

REDLINE=88171307; PubMed=3127527;

KRA Kipps T.J., Tonhave E., Chen P.P., Carson D.A.;

RA Kipps T.J., Tonhave E., Chen P.P., Carson D.A.;

RT "Autoantibody-associated kappa light chain variable region gene expressed in chronic lymphocytic leukemia with little or no somatic mutation. Implications for etiology and immunotherapy.";

RI J. Exp. Med. 167:840-852[1988]

CC -I- DISEASS: The protein is one of the surface immunoglobulin M cd. autoantibodies expressed in patients with chronic lymphocytic
                                                                                                                                                                                            Eukaryoča, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                      IG KAPPA CHAIN V-III REGION HAH,
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
JK1. SEGMENT.
BY SIMILARITY.
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                                                                                                                                                       01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
11-UUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-III region HAH precursor.
                                                                                                                                          129 AA
                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                        PIR; PLO022; K3HUHA.
HSSP; PR0362; LNTL.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0005955; P:immune response; NAS.
InterPro; IPR007110; IG-11ke.
KV2D HUMAN
KV1X HUMAN
KV1X HUMAN
KV1I HUMAN
KV1R HUMAN
KV5B MOUSE
KV5B MOUSE
KV3M MOUSE
KV1A HUMAN
KV1A HUMAN
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129 AA;
KV3L HUMAN P18135;
NON TER
SEQUENCE
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                                               5, 2004, 12:10:21 ; Search time 6.48731 Seconds (without alignments) 1139.758 Million cell updates/sec
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                                                                             US-10-044-569B-4
733
1 METPAQLLFLLLLWLPDTTG......TRLBIKGTVAAPSVFIFPFS 142
                                                                                                                                                                                                                                                                                   Description
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P01623 |
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Compugen Ltd.
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                                                                                                                                141681 segs, 52070155 residues
      GenCore version
Copyright (c) 1993 - 2004
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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KV3E
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Gaps

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Score 624; DB 1; Length 129; Pred. No. 1.3e-53; 4; Mismatches 4; Indels

85.1%; ilarity 93.8%; Conservative

Best Local Similarity Matches 120; Conserv

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Query Match

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PGQAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQKYGTSAITFG 120

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METPAQLLFLLLMLPDTTGEIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQK 60

1 METPAQLIFLILLWIPDTTGELALTQSPGTLSLSPGERATLSCRASQSFSSSYLAWYQOK

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=86041852; PubMed=2997711;
Klobeck H.G., Meindl A., Combriato G., Solomon A., Zachau H.G.;
"Human immunoglobulin kappa light chain genes of subgroups II and
                                                                                                         01-JAN-1988 (Rel. 06, Created)
10-JAN-1988 (Rel. 06, Last sequence update)
11-JAN-1998 (Rel. 38, Last annotation update)
12 kappa chain V-III region IARC/BL41 precursor.
                                         128 AA.
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                                         PRT;
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OGTKLEIK 127
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Homo sapiens (Human)
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61 PGQAPRLLIYGASTRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQKYGTSAITFG 120
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MEDINEL B8171307, PubMed=3127527;

Kipps T.J. Tomhave E., Chen P.P., Carson D.A.;

Kipps T.J. Tomhave E., Chen P.P., Carson D.A.;

Medicantibody-associated kappa light chain variable region gene expressed in chronic lymphocytic leukemia with little or no somatic mutation. Implications for etiology and immunotherapy.";

J. Exp. Med. 167:840-852(1988).

J. Exp. Med. 167:840-852(1988).

J. Dissass: The protein is one of the surface immunoglobulin M autoantibodies expressed in patients with chronic lymphocytic
                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1990 (Rel. 16, Created)
1-NOV-1990 (Rel. 16, Last sequence update)
15-UTU-1999 (Rel. 38, Last annotation update)
16 kappa chain V-III region HIC precursor.
18 kappa chain Sequence (Rel. 38, Last annotation)
19 kappa chain V-III region HIC precursor.
19 kappa chain N-III region HIC precursor.
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Pred. No. 1.2e-52;
5; Mismatches 5; Indels
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COMPLEMENTARITY-DETERMINING-1. FRAMENORK-2.
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FRAMEWORK-3.
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JK1 SEGMENT.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                               129 AA.
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HSSP; P80362; 1WTL.
GO; GO:0005576; C=xtracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
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Best Local Similarity 92.2%;
Matches 118; Conservative 5
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QGTKVEIK 128
                                                                                                         121 QGTRLEIK 128
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OGTKVEIK 128
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110 1
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129 AA,
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P18136;
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61 PGQAPRILIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQKYGTSAITFG 120
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PRAMEMOKK-1.
COMPLEMENTARITY-DETERMINING-1.
PRAMEMORK-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 128;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Indels
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86.7%; Pred. No. 3.6e-47;
.ive 5; Mismatches 11
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EMBL, 200021; CAA77316.1; -...
PIR; A01899; K3HU41.
HSSP; PO1607; IRJ
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR00110; Ig-like.
InterPro; IPR00110; Ig-like.
SMART; SM00406; Igv. 1.
PROSITE; PSS0835; IG_LIKE; 1.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Craniata, Vertebrata, Buteleostomi,
Catarrhini, Hominidae, Homo.
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MEDLINE=85087932; PubMed=6440122;
Pech M., Zachau H.G.;
"Immunoglobulin genes of different subgroups are interdigitated within the VK locus.";
Nucleic Acids Res. 12:9229-9236(1984).
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BY SIMILARITY.
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13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-III region VH precursor (Fragment).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 69.4%; Score 508.5; DB 1; Best Local Similarity 91.0%; Pred. No. 1.8e-42; Matches 101; Conservative 1; Mismatches 8;
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GO, GO:0005576; C:extracellular; NAS.
GO, GO:0005823; F:antigen binding; NAS.
GO, GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
FRM; PR0047; ig; I.
FMART; SM0406; IGv.
IRROSITE; PS50835; IG LIKE; I.
Immunoglobulin V region; Signal.
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PIR; A01900; K3HUVG.
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MEDLINE=85087932; PubMed=6440122;
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Mammalia, Eutheria, Primates,
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SEQUENCE
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P04434;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Bruppean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MEAPAQLLFLILLWLPDTTGEIVMTQSPATLSVSPGERATLSCRASQSVSNN-LAWYQQK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PGQPPRLLIYGASTRATGIPARFSGSGSGTEFTLTISRLQSEDFAVYCQQYNNWPPWTF
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                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=66177570; PubMed=3083417;
MIDLINE=66177570; PubMed=3083417;
MIDLINE=66177570; Curd J.G., Chen P.P.
Goldfien R., Carson D.A.;
"Cloning and sequence determination of a human rheumatoid factor
                                                                                                                                    Chordata; Craniata; Vertebrata; Euteleostomi;
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20-WAR-1987 (Rel. 04, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-lli region CLL precursor (Rheumatoid factor)
Homo sapiens (Human).
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FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 537; DB 1; Length 129;
Pred. No. 3.6e-45;
8; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
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JK1 SEGMENT.
BY SIMILARITY.
                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, bureze
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14275 MW; 5C13B411BE60CC14 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                 light-chain gene.";
Proc. Natl. Acad. Sci. U.S.A. 83:2195-2199(1986).
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(Rel. 05, Last sequence update)
(Rel. 38, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP, PR0362; IWTL.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003537; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam, Pro0047, ig; 1. SMART, SM00406, IGv; 1. SMO3165, SS00305, IG LIKE; 1. Immunoglobulin V region; Signal.
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129 1
129 AA;
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13-AUG-1987
15-JUL-1999
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Dischemistry 20:5816-5822(1981).

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PIR, AO1862, CASHUM.

HSSP, PR0362, 1WTL.

GO, GO:0003823, F: Rantigen binding; NAS.

GO, GO:0003823, F: Rantigen binding; NAS.

InterPro; IPR007110; Ig-like.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-82046598; PubMed-6794615;
Andrews D.W., Capra J.D.;
"Amino acid sequence of the variable regions of light chains from two
idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 EIALTOSPGTLSLSPGERATLSCRASOSFSSSYLAWYQQKPGQAPRLLIYGASTRATGIP
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21-JUL-1996 (Rel. 01, Last sequence update)
15-JUL-1998 (Rel. 38, Last annotation update)
16-JUL-1999 (Rel. 38, Last annotation update)
17-JUL-1999 (Rel. 38, Last annotation Wol. 16 kappa chain V-III region Wol.
18 kappa chain (Human).
18 Bukaryota; Matazoa, Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81 DRFSGSGSGTDFTLTISRLEPEDFAVYYCOKYGTSAITFGQGTRLEIK 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  68.9%; Score 505; DB 1; Length 109; 88.9%; Pred. No. 3.7e-42; ive 8; Mismatches 4; Indels
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larity 88.9%; Pred. No. 7.2e-42;
Conservative 5; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                           109 AA; 11775 MW; 7689C3ECD646FFB4 CRC64;
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                        GO; GO: 000557, C: extracellular; NAS. GO; GO: 0003823; F: antigen binding; NAS. GO; GO: 0006955; P: immune response; NAS. InterPro; IPR007110; Ig-11ke.
InterPro; IPR007110; Ig-11ke.
PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS50835; IG_LIKE; 1.
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SWART; SW00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region.
DISULFID 23 89 BY
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Best Local S:
Matches 96
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KV3E HUMAN
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Pech M., Zachau H.G.;
within the VK locus.";
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within the VK locus.";
Nucleic Acids Res. 12:9239-9236(1984).

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      group.";
Biochemistry 20:5816-5822(1981).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULLN ACTIVITY.
PIR; A01892; K3HUSI.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 kappa,chain V-III region SIE.
Homo sapiens (Human).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primatee; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 PGQAPRLLIYGASTRATSIPARFSGSGSGTDFTLTISSLQPEDFAVYXCQQ 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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FRAMEWORK-1.
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COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
BY SIMILARITY.
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88.3%; Pred. No. 3.2e-42;
ive 3; Mismatches 10; Indels
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98; Conservative
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21-JUL-1996 (Rel. 01, Last sequence update)
15-JUL-1998 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 kappa chain V-III region B6.
17 kappa chain V-III region B6.
18 kappota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI TaxID=9606,
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DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSLGRTFGQGTKVEIK 108
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                                                                                             21-JJJ-1986 (Rel. 01, Created)
21-JJJ-1986 (Rel. 01, Last sequence update)
15-JJJ-1999 (Rel. 38, Last annotation update)
IG kappa chain V-III region Ti.
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Best Local Similarity
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P01619;
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MewKirk M., Chen P.P., Carson D.A., Posnett D., Capra J.D.;
NewKirk M., Chen P.P., Carson D.A., Posnett D., Capra J.D.;
NewKirk M., Chen P.P., Carson D.A., Posnett D., Capra J.D.;
In "Amino acid sequence of a light chain variable region of a human
reactivity with antipeptide antibodies.";
In Mol. Immunol. 23:139-244(1986).
Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson Melson 
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66.7%; Score 489; DB 1; Length 10
82.4%; Pred. No. 1.3e-40;
ive 11; Mismatches 8; Indels
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20-MAR-1987 (Rel. 04, Last sequence update)
20-MAR-1989 (Rel. 38, Last annotation update)
19 kappa chain V-III region GOL (Rheumatoid factor).
Homo sapiens (Human).
-1- MISCELLANEOUS: This is a Bence-Jones protein. PIR, A01891; K3HUB6.
HSSP; A80362; 1HTL.
InterPro; IPR00710; IG-like.
                                                                                                                                                                  SMART; SM00406; 19.".

SMART; SM00406; 169; 1.

PROSITE; PS50835; 1G LIKE; 1.

Immunoglobulin V region; Bence-Jones protein.

NON TER 108 108

SRQÜENCE 108 AA; 11635 MW; BEC14FF07A419E
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Best Local Similarity 82.4%
Matches 89; Conservative
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P04206;
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ACC HUMAN
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a small family of germ-line V genes.";

Nature 307:77-80(1984).

"I MISCELLAREOUS: THIS GENE WAS ISOLATED FROM THE NG9/9.1 HYBRIDOMA.
IF MISCELLAREOUS: THIS GENE WAS ISOLATED FROM THE NG9/9.1 HYBRIDOMA.

PIR, A01894; K3HUNG.

GO; GO:0005576; C:extracellular; NAS.

GO; GO:0005576; C:extracellular; NAS.

GO; GO:0005576; F:antigen binding; NAS.

GO; GO:0006955; F:antigen binding; NAS.

RO; GO:0006955; F:antigen binding; NAS.

RO; GO:0006955; F:antigen binding; NAS.

RO; GO:0006955; F:antigen binding; NAS.

RO; GO:0006955; F:antigen binding; NAS.

RO; GO:0006955; F:antigen binding; NAS.

RO; GO:0006955; F:antigen binding; NAS.

RO; GO:0006955; F:antigen binding; NAS.

"Manunoglobulin V region; Signal; Hybridoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62
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MEDIINE=76276460; PubMed=60899;
MEDIINE=76276460; Capra J.D.;
Mapper D.G., Capra J.D.;
"The amino acid sequence of the variable regions of the light chains from two idiotypically cross reactive IgM anti-gamma globulins.";
Ann. Immunol. (Faris) 127C:261-271(1976).
-! MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 SGEIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGATSRATG
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                            21-JUL-1996 (Rel. 01, Created)
15-JUL-1996 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 kappa chain V-III region NG9 precursor (Fragment).
17 Memo sapplens (Human).
18 Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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BY SIMILARITY.
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27 93 BY SIMILARITY.
100 100 W, 5D9AF363CC52632F CRC64;
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16-OCT-2001 (Rel. 40, Last annotation update)
19 kappa chain V-III region POM.
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SEQUENCE FROM N.A.
MEDLINE=84093600; PubMed=6419127;
Bentley D.L.;
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21-JUL-1986 (Rel. 01, Last seq
16-OCT-2001 (Rel. 40, Last ann
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KV3F HUMAN
P01624;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 EIALTOSPGTLSLSPGERATLSCRASOSFSSSYLAWYQQXPGQAPRLLIYGASTRATGIP 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

KIODECK H.G., Combriato G., Zachau H.G.;

KIODECK H.G., Combriato G., Zachau H.G.;

"Immunoglobulin genes of the Kappa light chain type from two human
"Immunoglobulin sa closely related.";

Nucleic Acids Res. 12:6995-7006(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
16 kappa chain V-I region Walker precursor.
17 kappa chains (Human).
18 bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
18 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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PRAMENORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMENORK-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                             109 AA; 11922 MW; 62821DDC6A8ABA86 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                    13;
                                                                                                                                                                                                                                                                                                                                                                           Score 447; DB 1;
Pred. No. 1.5e-36;
8; Mismatches 13;
                                                                                                                                                                                                                                                                         BY SIMILARITY
HSSP, PRO362; INTL.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0006955; F:antigen binding; NAS.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR007110; Ig-11ke.
Ffan; PR00047; ig; I.
SWART; SW00406; IGv; I.
Immunoglobulin V region.
DISGURIO 23 89 BY SIMILARITY
NON TER 109 AA; 11922 MW; 62821DDC6AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X00965; CAA25477.1; ALT_TERM.
PTR; A01883; K1HUWK.
HSSP; PO1607; IREI.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0006955; F:antigen binding; NAS.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003596; Ig-V.
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Pfam; PR00047; ig; 1.
SMARY; SM04006; IGv; 1.
PROSITE; PSS0835; IG LIKE; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                              61.0%;
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Matches 87; Conservative
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                                                                                                                                              1;
                                                                                                                                                                                                                                               61 PGQAPRILIYGASTRATGIPDRFSGSGSTDFTLTISRLEPEDFAVYYCQKYGTSAITFG 120
                                                                                                                                                                       1 METPAQLLFLLLLWLPDTTGEIALTQSPGTLSLSPGERATLSCRASQSFSSSYLAWYQQK 60
                                                                                                                                                                                      1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 07, Last sequence update)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-IV region B17 precursor.
Home sapiens (Human).
Edwaryotta, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Marsh P., Mills F., Gould H.;
"Detection of a unique human V kappa IV germline gene by a cloned cDNA probe."
                                                                                                                DB 1; Length 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IG KAPPA CHAIN V-IV REGION B17.
PRAMENORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
             FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
BY SIMILARITY.
COMPLEMENTARITY-DETERMINING-2,
                                                                                                                58.3%; Score 427.5; DB 1; Length 66.4%; Pred. No. 1.4e-34; Live 16; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Marsh P.; Submitted (OCT-1986) to the EMBL/GenBank/DDBJ databases.
                                                                                    14069 MW; F941FA07D4AFC2F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0005576; C:extracellular; NAS. GO; GO:0003823; F:antigen binding; NAS. GO; GO:000695; P:immune response; NAS. InterPro; IPR007110; IG-11ke.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic Acids Res. 13:6531-6544 (1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=86041854; PubMed=2997713;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
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HSSP; P80362; 1WTL.
                                                                                                             Query Match
Best Local Similarity 66.4%
Matches 85; Conservative
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129
110
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120
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P06314;
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61 WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYNL 120
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                                                                                                                                                   5; Gaps
                                                                                                                   ch 57.4%; Score 420.5; DB 1; Length 134; l Similarity 60.9%; Pred. No. 7.1e-34; B1; Conservative 20; Mismatches 27; Indels 5:
                FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
 COMPLEMENTARITY-DETERMINING-2
82 COMPLEMENTARITY-DETERMINING-
114 FRAMEWORK-3.
121 COMPLEMENTARITY-DETERMINING-
133 FRAMEWORK-4.
114 BY SIMILARITY.
134 A: 14966 MW; 6413A22FD0738832 CRC64;
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134 AA;
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Search completed: April 5, 2004, 13:24:55 Job time: 6.48731 secs

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Q9UL70 Q91WF8 Q91W79 Q9UL77 Q9UL77 Q9UL77 Q9UL81 Q9UL81 Q9UL81 Q9UR9 Q91WS9 Q91

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[1] _____SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDILINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-WAY-2000 (TrEMBLrel. 13, Created)
1-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fetus.',
Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL, AR05015036, AAD56272.1; -.
PIR, A30601 A30601.
PIR, A30601 B30601.
PIR, B30601 B30601.
PIR, B30601, B30601.
PIR, B30601, C30601.
PIR, C30601, C30601.
PIR, C30601, C30601.
PIR, C30601, C30601.
PIR, C30601, C30601.
PIR, B30601, B30601.
PIR, B30601, B30601.
PIR, B30601, B30601.
PIR, B30601, B30601.
PIR, B30601, F30607.
PIR, B30601, F30608.
PIR, B30601, F30608.
PIR, B30601, B30608.
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Bukaryota; Metazoa; Chordata;
Mammalia; Butheria; Primates;
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                                           NCBI_TaxID=9606
                                                                                                                                                                                                                                 (Fragment)
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Q9UL78
ID Q9UL78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q94178 homo sapien
Q74473 homo sapien
Q72473 homo sapien
Q72344 homo sapien
Q8tcd0 homo sapien
Q8tcd0 homo sapien
Q78135 homo sapien
Q78183 homo sapien
Q7183 homo sapien
Q7184 mus musculu
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733
1 METPAQLLFLLLLMLPDTTG.....TRLEIKGTVAAPSVFIFPPS 142
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              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Sp_archea:*

Sp_archea:*

Sp_fung1:*

Sp_human:*

Sp_nuvertebrate:*

Sp_mort

Sp_mort

Sp_nuvertebrate:*

Sp_nuvertebrate:*

Sp_rorganelle:*

Sp_phage:*

Sp_phage:*

Sp_rorganelle:*

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sp_bacteriap:*
sp_archeap:*
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seg length: 200000000
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Match 1
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Perfect score:
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Maximum DB
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No.
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Craniata, Vertebrata, Euteleostomi, Catarrhini, Hominidae, Homo.

109 AA

PRT;

ALIGNMENTS

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14; Mismatches
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InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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  98; Conservative
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SEQUENCE FROM N.A.
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Q9UL86
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X Strausberg R.L., Feingold E. R., Grouse L.H., Derge J.G.,

A Strausberg R.L., Feingold E. R., Grouse L.H., Derge J.G.,

A Strausberg R.L., Feingold E. R., Grouse L.H., Derge J.G.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Mullahy S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Richards S., Worlby K.C., Hale S., Garcia A.M., Galber B.H.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Rares S. R. M. Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

A Norrand M. M. A. M. A. M. A. M. A. M. A. M. A., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Nameron M. M. M. A. M. Schmutz J., Myers R.M., Butterfield Y.S.,

A Maray D.M. Salaska U., Smailus D.E., Schnerch A., Schein J.E.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                  21 EIALTOSPGTLSLSPGERATLSCRASOSFSSSYLAWYQQKPGQAPRLLIYGASTRATGIP
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                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 3e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DRFSGSGSGTDFTLTISRLEPEDCAVYYCQQYGSSPLTFGGGTKVEIK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81 DRFSGSGSGTDFTLTISRLEPEDFAVYYCOKYGTSAITFGOGTRLEIK 128
                                                                                                                                                                                                                                                                                                                                 Length 109;
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                                                                                                                                                                                                                                                  109 109
109 AA; 11646 MW; SF675C52EC7EE197 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 25, Created)
(TrEMBLrel. 25, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                           Score 505; DB 4; L
Pred. No. 1.1e-44;
5; Mismatches 5;
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                          PIR; PH0965; PH0965.
PIR; S34096; S34096.
HSSP; P80362; JWTL.
INTEATRO; IPR007110; Ig-like.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; Ig; 1.
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PROSITE; PS50835; IG_LIKE; 1.
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89.8%;
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Best Local Similarity
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01-OCT-2003 (
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NON TER
SEQUENCE
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Q7Z473;
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60 PGKAPQILIYAASTIQSGVPSRFSGSASGTDFTLSISCLQSEDFATYYCQQYYTYPWTFG 119
                                                                                                                                                    61 PGQAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQKYGTSAITFG 120
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                                               1 METPAQLIFILLIMIPDITGEIALTQSPGTLSLSPGERATLSCRASQSFSSSYLAMYQQK
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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01-007-2003 (TrEMBLrel. 25, Last sequence update)
01-007-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Hypothetical Screin.
Hypothetical Chordinan).
Bukaryota Metazoa; Chordinan,
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin kappa chain variable region
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Pred. No. 3.2e-43;
6; Mismatches 8; Indels
29; Indels
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EMBI, APOSIOSE, AADSECSE, ABOSECSE, 1; -.
PIR; B30607; B30607.
PIR; I30601; I30601.
                                                                                                                                                                                                                                                                                                                                                                                                                                               109 AA
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01-MAY-2000 (TrEMBLrel. 13, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
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                                                                                                                                                                                                                                                              121 OGTRLEIKGTVAAPSVFIFPPS 142
                                                                                                                                                                                                                                                                                             120 QGTKVEIKRTVAAPSVFIFPPS 141
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57 YQQXPQQAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQKYGTSA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 YLQKPGQSPQLLIYLGSNRASGVPDRPSGSGSGTDFTLKISKVBAEDVGIYYCMQGLQTP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata, Vertebrata, Buteleostomi,
Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                      4.
                                                                                                                                                                                                                                                                          / Match
Local Similarity 62.3%; Score 466; DB 4; Length 239;
Local Similarity 62.3%; Pred. No. 3.6e-40;
les 91; Conservative 23; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 239
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58.9%; Pred. No. 1.6e-38;
ive 27; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
TISSUB-Lung;
TISSUB-Lung;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC02362; AAH22362.1; -.
PIR; S42267; S42267.
PIR; S42267; S42267.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR007110; Ig-like.
InterPro; IPR00306; Ig_MHC.
InterPro; IPR003596; Ig_V.
InterPro; IPR003596; Ig_V.
SWART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS00290; IG_MHC; 1.
PROCHELICAL DROCHO.
SEQUENCE 239 AA; 26234 MW; FACEDC3A3B03B71D CRC64;
InterPro; IPR003597; Ig_c1.
InterPro; IPR003506; Ig_YMC.
InterPro; IPR003506; Ig_YW.
Pfam; PF00047; ig; 2.
SWART; SW00407; IGc1: 1.
PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS0090; IG_MRC; 1.
SROCHERIAL PROCE CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL C
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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nes 86; Conservative
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Q8TCD0
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                                                                                                                   61 PGQAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQKYGTSAITFG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 MRVLAQLLGLLLCFFGARCDIQMTQSPSSLSASVGDTVTITCRASQDI-SNYLAWFQQK 61
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Hypothetical protein.
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC030814; AAH30814.1; -.
PIR; S23638; S23638.
PIR; S34091; S34091.
PIR; S40357; S40357.
InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.; Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases. EC05332; AAH05332.1; -. Hypothetical protein. SEQUENCE 236 AA; 25702 MW; 7FBFE4ED23084BC6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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MEDLINE=22388257; PubMed=12477932;
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es 93, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                         SEQUENCE FROM N.A
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QBNEKO;
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121 STFGQGTKLEIKRTVAAPSVFIFPPS 146

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Wu X., Liu E
Young D.C.;
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                                            09UL83
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09UL85
RESULT 8
Q9UL83
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                                                                                                                                                                                                                                              Eukaryota, Metazoa; Chordata; Craniata; Vertebrata, Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 13; Length 237;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Klein S., Strausberg R.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC054155; AAH54155.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
SEQUENCE 237 AA; 26300 MW; 47BBD0D2639CB436 CRC64;
                                                                                                                      Created)
Last sequence update)
Last annotation.update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                   01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last seq
01-0CT-2003 (TrEMBLrel. 25, Last ann
Mypothetical protein.
Xenopus laevis (African clawed frog)
                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22341132; PubMed=12454917;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dev. Dyn. 225:384-391(2002)
                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                   Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                    FROM N.A.
                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=8355;
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Best Local Si
Matches 85;
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Eukarota, Metazona,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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ferus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                     "Myosin-reactive autoantibodies in rheumatic carditis and normal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQKYGTSAITFGQGTRLEIK 128
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                                                                                                                                                                                                                                                                                                                                                            Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin kappa chain variable region
                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108 AA; 11834 MW; 9F9C5A92EBA96EEA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 57.9%; Score 424.5; DB 4; Local Similarity 78.7%; Pred. No. 2.5e-36; es 85; Conservative 8; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clin. Immunol. Immunopathol. 87:184-192 (1998).
EMBL, AF035031; AAD56267.1; -.
EMBL, AF035031; AAD56267.1; -.
PIR, B30609; B30609.
PIR, D30609; D30609.
PIR, S34099; S34099.
PIR, S34099; S34099.
HSSP, P80362; 1WTL.
InterPro; IPR007110; Ig-like.
InterPro; IPR00356; Ig-v.
Pfam; PR0047; ig/1.
SWART; SM00406; IGy. 1.
PROSITE; PS50835; IG_LIKE; 1.
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                                                                                                                                                                                                                                                                                                                                              MEDLINE=98277139; PubMed=9614934;
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PRELIMINARY;
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                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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61 PGQAPRLLIYGASTRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQXYGTSAITFG 120
                                                                                                                             57 YQQKPGQAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQKYGTSA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 METPAQLIPLILIMIPPITGETALIQSPGTLSLSPGERATLSCRASQSF----SSSYLAW 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (1)
SEQUENCE FROM N.A.
SEQUENCE R.;
SEQUENCE R.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC002035; AAH02035.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .l protein.
238 AA; 26344 MW; FB2B06A0B801330A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                 238 AA.
                                                                                                                                                                                            121 QGTRLEIKGTVAAPSVFIFPPS 142
                                                                                                                                                                                                                   ||:|||| |||||
122 SGTKLEIKRADAAPTVSIFPPS 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PDB; 1191; 25-DEC-02.
PDB; 1LO2; 31-JUL-02.
PDB; 1LO4; 31-JUL-02.
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$24536; $24536.
$24538; $24538.
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C32248; (
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S24500;
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S24529;
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S24533;
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Matches
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PIR;
PIR;
POB;
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KX MEDLINE-2238827; PubMed=12447932;

KR Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

KIAUSARIS R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,

KA Alteschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Alteschul S.F., Joedan H., Moore T., Max S.I., Wang J., Heich F.,

RA Alteschul S.F., Joedan H., Moore T., Max S.I., Wang J., Heich F.,

RA Distchench M., Scares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Sapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gabb R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,

Willalon D.K., Muzny D.M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Sheychenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Unes S.J., Marram M.A.,

Machine S.J., Marram M.A.,

Rad mouse CDNA sequences.",

Tand mouse CDNA sequences.",
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                                                                                                                                                                                                                                                                                                                                                                               2; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARFSGSGSTEFTLTISSLQSEDFAIYHCQQYNSWPPLTFGGGTKVEIK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                       81 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQKYGT-SAITFGQGTRLEIK 128
                                                                                                                                                                                                                                                           Query Match 57.6%; Score 422; DB 4; Length 109; Best Local Similarity 77.1%; Pred. No. 4.7e-36; Matches 84; Conservative 12; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC055906; AAH55906.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypochetical protein.
SEQUENCE 236 AA; 26299 MW; 0DB03489AAA6396F CRC64;
                                                                                                                                                                                                                 109 AA; 11761 MW; FB1E43E7C7AFACCC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
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STRAIN=CZECH II; TISSUE=Breast tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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                                  HSB), P80362; 1WTL.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
Fram; PF00047; ig; 1.
SWART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
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01-0CT-2003 (TrEMBLrel. 25, Cr
01-0CT-2003 (TrEMBLrel. 25, La
01-0CT-2003 (TrEMBLrel. 25, La
Rypothetical protein.
Mus musculus (Mouse).
EMBL; AF035029; AAD56265.1;
PIR; D30609; D30609.
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ses 80; Conserva
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SEQUENCE
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Gaps

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PRT;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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nes 79; Conservative
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PIR, S16112, S16112.
PIR, S26334, S26334.
PIR, S53750, S53750.
                                                                                                                                                              PH0106.
PH1030.
PH1031.
                                                                                                                                                                                                                            PH1034
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                                                                                                                                                                                      PH1030;
PH1031;
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PT0359;
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                                                                                                     E28833;
                                                                                                                           F32530;
                                                                                                                                                                                                                            PH1034;
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SEQUENCE 2:
                                                                                                                                            H31485;
                                                                                                                                                                PH0106;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 PGKSPKTLIYRANRLVDGVPSRFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPRTFG 121
60 YLQKFQQSPKILIYKVSNRFSGVPDRFSGSGSGTDFTIKISRVEAEDLGVYYCFQGSHVP 119
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                                                                                                                                                                                                                                               01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Anti-colorectal carcinoma light chain.
Anti-colorecta, Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalla, Eutheria, Rodentia, Sciurognathi; Muridae, Murinae, Mus.
102B_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

MEDLINE-3183497. PubMed=8372513;

MEDLINE-9383497. PubMed=8372513;

Tonge D. Hennam J.F., Greene A.R., Lee I.D., Edge M.D.;

"Cloning and characterization of 1116NS19.9 heavy and 11ght chain cDNAs and expression of antibody fragments in Bscherichia coli.";

EMBL; S65921; AAB28160.1; -.

SEQUENCE 236 AA; 26454 MW; 2C586EBF5EA1074C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56.3%; Score 412.5; DB 11; Length 236; 56.3%; Pred. No. 1.3e-34; ive 22; Mismatches 39; Indels 1;
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Last annotation update)
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                                                                  117 ITFGOGTRLEIKGTVAAPSVFIFPPS 142
                                                                                          120 YTFGSGTKLEIKRADAAPTVSIFPPS 145
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122 GGTKLEIKRADAAPTVSIFPPS 143
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Q8VCI6 01-MAR-2002 (TrEMBLrel. 20, C3
01-MAR-2002 (TrEMBLrel. 20, L6
01-OCT-2003 (TrEMBLrel. 25, L6
Hypothetical protein.
Mus musculus (Mouse).
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Submitted (DEC-2001) to the
EMBL; BC019760; AAH19760.1;
PIR; A27887; A27887.
PIR; A32248; A32248.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80; Conservative
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B27887; B27887.
B30577; B31687.
B31485; B31485.
B32248; B32248.
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SEQUENCE FROM N.A.
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Q7TS98;
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57 YOOKPGOAPKLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCOKYGTSA 116
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                                                                                                                                                                                                                                1 METPAQLIFILLIWLPDTTGEIALTQSPGTLSLSPGERATLSCRASQSF----SSSYLAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                               55.5%; Score 406.5; DB 11; Length 238; 54.1%; Pred. No. 5.3e-34; ive 29; Mismatches 33; Indels 5;
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Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
BMBL; BC019474; AAH19474.1; -.
PIR; B47329; B47329.
InterPro; IPR007010; Ig-like.
InterPro; IPR00306; Ig-WC.
InterPro; IPR00306; Ig-W.
Pfam; PF00047; Ig; 2.
SMART; SMO0406; IGv; 1.
PROSITE; PS50835; IG-LIKE; 2.
PROSITE; PS00890; IG-LIKE; 2.
Hypothetical protein.
1 protein.
238 AA; 26224 MW; 35EC08E3DE5414AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     234 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 PTFGGGTKLEIKRADAAPTVSIFPPS 145
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Mon Apr 5 14:16:19 2004
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234 AA; 25702 MW; 102551C58AC2FA9F CRC64;

SEQUENCE

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118-110-044-3670-4.rspt

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1 METPAQLIFILILIWIPDITGEIALTQSPGTLSLSPGERATLSCRASQSFSSS----YLAW 56
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Query Match 55.3%; Score 405.5; DB 11; Length 234; Best Local Similarity 57.7%; Pred. No. 6.6e-34; Matches 82; Conservative 18; Mismatches 41; Indels 1;
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Submitted (GAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC021781; AAH21781.1;
EMBL; BC021781; AAH21781.1;
PDB; IKC5; 24-JUL-02.
GO; GO:005576; C:extracellular; IEA.
GO; GO:0015070; F:toxin activity; IEA.
R GO; GO:0015070; F:toxin activity; IEA.
R GO; GO:0015070; F:toxin activity; IEA.
R InterPro; IPR004124; GONCOXIN.
R InterPro; IPR00410; IG-like.
R InterPro; IPR003006; IG-MHC.
R InterPro; IPR003006; IG-MHC.
R Ffam; PF0256; Conotoxin; 1.
R Ffam; PF00047; IG; 2.
R Ffam; PF00040; IG; 2.
R FAMRT; SM00406; IGV; 1.
R PROSITE; PS50835; IG-LIKE; 2.
R PROSITE; PS50835; IG-LIKE; 2.
R PROSITE; PS00830; IG-LIKE; 2.
R HYPOCHELICAL Drotein.
W HYPOCHELICAL Drotein.
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TISSUE=Colon;
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Q8VC55
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April 5, 2004, 12:09:21 ; Search time 45.8917 Seconds (without alignments) 874.270 Million cell updates/sec
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1 METPAQILFLLLLMLPDTTG.....TRLEIKGTVAAPSVFIFPPS 142
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

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1: _geneseqp1980s:*
3: _geneseqp2000s:*
4: _geneseqp2001s:*
5: _geneseqp2001s:*
6: _geneseqp2003s:*
7: _geneseqp2003bs:*
8: _geneseqp2003bs:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Abp57366 Anti-TRAI Abr41862 Human DIT Ada43061 Human ant Aar38673 F105VK-F1 Aar41286 F105 rear Add01127 Human imm Aag71272 Human imm	Human Human Human Immuno	Aau14462 Human nov Aau14461 Human nov Aau14461 Human nov Aau14464 Human nov Aao14066 Light cha	Human Novel Human
ABPS7366 ABR41582 ADA43061 AAR38673 AAR41286 ADD01357 AAG71272	ABG63490 ADC61062 AAM24101 AAR52951	AAU14462 AAU14463 AAU14461 AAU14464 AAO14066	ABU08018 AAU33249 AAR38650
	238 388 388 44 723 74 74 75 75 75 75 75 75 75 75 75 75 75 75 75		
883.9 83.9 82.1 82.1 82.1 82.0 8.2 9.0	8889 6.18 6.08 6.08 6.08	0 0	80.4 79.5 78.3
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ALIGNMENTS

RESULT 1

Monoclonal antibody; variable region; heavy chain; light chain; VH; complementarity determining region; CDR; MAb; BO2C11; conformational epitope; factor VIII; KRIXI; von Willebrand factor; hemostasis; intravacular coequiation; arterial thrombosis; arterial restenosis; venous thrombosis; arteriosclerosis. Light chain variable region VL of BO2C11. Location/Qualifiers Æ AAB47060 standard; protein; 142 43. .54 /label= CDR1 69. .75 /label= CDR2 109. .117 /label= CDR3 99GB-00016450. 13-JUL-2000; 2000WO-EP006677 (LEUV-) LEUVEN RES & DEV VZW. (first entry) WO200104269-A1 14-JUL-1999; 14-JUL-1999; Homo sapiens 08-MAY-2001 18-JAN-2001 AAB47060; Key Domain Domain Domain XSXETETETETETEXSXERXEXEXEXEXEXEXEXEXEXEXEXEXEX

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Jacquemin MG, Saint-Remy JR; WPI; 2001-138333/14. N-PSDB; AAC85453. Novel call lines for producing monoclonal antibodies that bind to factor involved in hemostasis and coagulation cascade, useful for treating and preventing coagulation disorders.

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Example 5; Fig 7; S5pp; English

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Homo sapiens,
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This sequence represents the light chain variable region of the human monoclonal antibody (MAb), BO2C11. BO2C11 is a human MAb which recognises a conformational epitope within the carboxy-terminal of the factor VIII light chain. BO2C11 recognises both the wild type and Arg1s0fils factor VIII light chains. The MAb produced by the cell line of the invention, KRIXI, specifically recognises the wild type factor VIII light chains. The MAb produced by the cell line of the invention, KRIXI, can be used to inhibit the brinding of factor VIII light chain. Second to inhibit the brinding of factor VIII light chain. The mew cell line KRIXI, is deposited with the Belgian Coordinated Collections of Micro-organisms, under accession number LMBP 5089CB. KRIXI, or fragments of it, optionally with a thrombolytic agent, are useful for the treatment and/or prevention of hemostasis, coagulation disorder thrombolic pathologic condition such as intravascular coagulation, arterial thrombosis, arterial restensis, venous thrombosis or arteriosclerosis, and attenuation of coagulation in ammmal. An effective and safe antithrombotic therapy is provided which reduces the risk of bleeding in mammals, more particularly in humans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, antibody; B02C11; KRIXI; light chain; heavy chain; inflammation; variable region; factor VIII inhibitor; sepsis; septic shock; thrombus formation; systemic inflammatory response syndrome; CDR, disseminated intravascular coaquiation; haemophilia A; immunosuppressive; complementarity determining region; antibacterial; antihilammatory.
                                                                                                                                                                                                                                                                                                                                           PGQAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQKYGTSAITFG 120
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                                                                                                                                                                                                                                                                                           METPAQLLFLLLLWLPDTTGEIALTQSPGTLSLSPGERATLSCRASQSFSSSYLAWYQQK
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                                                                                                                                                                                                                                          Length 142;
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                                                                                                                                                                                                                                          100.0%; Score 733; DB 4;
100.0%; Pred. No. 2.9e-42;
cive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human B02C11 light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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/label= CDR1
69. .75
/label= CDR2
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/label= CDR3
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Best Local Similarity 100.
Matches 142; Conservative
                                                                                                                                                                                                                   Sequence 142 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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The present invention relates to a pharmaceutical composition for the prevention and/or treatment of systemic Inflammatory response syndrome (SIRS), espsis, septic shock, thrombus formation in the microvasculature and disseminated intravascular coagulation in mammals, comprising as an active ingredient a partial inhibitor of factor VIII, in admixture with a cartive intractions may include the antibodies B02011 and KRIXI. The present sequence is the light chain variable region of B02011
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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                         Pharmaceutical composition for treating systemic inflammatory response syndrome, sepsis, septic shock and/or thrombus formation in microvasculature in mammals, comprises a partial inhibitor of factor VIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 METPAQLIFLILIMIPDITGELALIQSPGTLSLSPGERATISCRASQSFSSSYLAWYQOK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 METPAQLLFLLLMLPDTTGELALTQSPGTLSLSPGERATLSCRASQSFSSSYLAWYQQK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 733; DB 5;
100.0%; Pred. No. 2.9e-42;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The kappa chain of immunoglobulin clone 4.1.1.
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                                                                                                                                                                                                         Disclosure; Fig 11; 41pp; English
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Best Local Similarity 100.
Matches 142; Conservative
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N-PSDB; AAL49255
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                                       The present sequence represents a kappa chain of an antibody of the invention. The antibody is directed cytotoxic T-lymphocyve antiplen (CTLA) and Antibodies of the invention are composed of a heavy chain variable region, comprising a modified contiguous sequence from a FRI-FR3 sequence encoded by a human VH3-33 family gene. The modifications are contained in CDR1, CDR2 and/or framework regions. The antibodies may be used to inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity disorders (e.g. cancer). CTLA-4 stimulatory agents may be used to used to upoliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be used to upoliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be used to up-regulate immune system to up-regulate immunodeficient
                                                                                                                                                                                                                                                                                61 PGQAPRILIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQKYGTSAITFG 120
                                                                                                                                                                                                                                                                                             61 PQQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSPWTFG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel antibodies capable of binding cytotoxic T-lymphocyte antigen (CTLA)
                                                                                                                                                                                                                                      1 METPAQLIFILILMIPDITGELALTQSPGTLSLSPGERATLSCRASQSFSSSYLAWYQQK 60
                                                                                                                                                                                                                                                          1 METPAQLIFILILIWIPDITGEIVIJOSPGTLSLSPGERATLSCRASQSISSSFLAWYQQR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system; hyperimmunity disorder; autoimmune disease; diabetes; graft rejection; proliferative disorder; cancer; immunodeficient disorder.
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                                                                                                                                                                                                                  5; Indels
                                                                                                                                                                                             Score 682; DB 3;
Pred. No. 1.2e-38;
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                                                                                                                                                                                                     Pred. No. 1.26
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "signal peptide"
                                                                                                                                                                                                                                                                                                                           OGTRLEIKGTVAAPSVFIFPPS 142
                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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e.g. immune disorders.
                    Claim 3; Fig 1A; 157pp; English.
                                                                                                                                                                                             93.0%;
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Matches 131, Conservative
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N-PSDB; AAA46893.
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                                                                                                                                                                        Sequence 235 AA;
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treating,
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                                                                                                                                                                                             Query Match
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Peptide
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invention. The antibody is directed cytocoxic T-lymphocyte antigen (CTLA)

4. Antibodies of the invention are composed of a heavy chain variable region, comprising a modified contiguous sequence from a RRI-FR3 sequence encoded by a human VH3-33 family gene. The modifications are contained in CDR1, CDR2 and/or framework regions. The antibodies may be used to inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity disorders (e.g. autoimmune disease, diabetes and graft rejection) and proliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be used to up-regulate immune system to up-regulate immunodeficient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 PGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSPWTFG 120
                                                                                                              The present sequence represents a kappa chain of an antibody of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PGGAPRILIYGASTRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQKYGTSAITFG 120
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-4 containing specified heavy and light chain sequences, useful for treating, e.g. immune disorders.
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Pred. No. 1.2e-38;
6; Mismatches 5; Indels
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/label= Signal_peptide
21. .235
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                                                                                   Claim 3; Fig 22g; 157pp; English.
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larity 92.3%;
Conservative
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N-PSDB; AAD54344.
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Best Local Similarity
Matches 131; Conser
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Bedian V, Gladue RP,
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                                                                      The invention relates to the use of human anti-cytotoxic T lymphocyte antigen-4 (anti-cyTLA-4) antibody in the preparation of a medicament for the treatment of cancer such as bone cancer, pancreatic cancer, skin cancer, cutaneous or intraocular malignant melanoma, uterine and ovarian cancer, cancer of the anal region, stomach cancer, breast cancer testicular cancer uterine cancer and carcinoma of the fallopian tubes. The present sequence is human anti-CTLA-4 antibody kappa chain
                                                                                                                                                                                                                                                                                                                                                                           1 METPAQLIFILIMIEPDITGEIVITQSPGTISISGERATISCRASQSISSFLAWYQQR 60
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                                                                                                                                                                                                                                                                       Length 235;
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preparation of medicament for the treatment of cancer.
                                                                                                                                                                                                                                                                       Score 682; DB 6; L
Pred. No. 1.2e-38;
6; Mismatches 5;
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/note= "variable region"
129. .235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QGTRLEIKGTVAAPSVFIFPPS 142
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                                     Disclosure; Fig 1G; 76pp; English.
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                                                                                                                                                                                                                                                                     93.0%; 5
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Best Local Similarity 92.3
Matches 131; Conservative
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/note=
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                                                                                                                                                                                                                                   Sequence 235 AA;
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Peptide
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                                            The invention relates to antibodies that interact with osteoprotegerin ligands (OPGL). The antibody is useful for detecting the level of OPGL in a biological sample. The antibody, or the pharmaceutical composition comprising the antibody, or the pharmaceutical composition an inflammatory condition with attendant bone loss, an autoimmune condition with attendant bone loss in a patient or rheumatoid arthritis in a patient. In particular, the antibody or composition is useful for treating bone diseases, e.g. osteoporosis, bone loss from arthritis. Paget's disease, osteopenia, endocrine osteoporosis (e.g. Cushing's syndrome or acromegaly), osteogenesis imperfecta, homocystinuxia, Menkes' syndrome, Xiley-Day syndrome, osteomyelitis, hypercalcemia, or natioody kappa light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New chimeric or human monoclonal antibody or its antigen-binding portion that specifically binds to and activates human CD40, useful for enhancing an immune response in a human, or treating cancer, HIV, neutropenia or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 666; DB 6; L. Pred. No. 1.5e-37; 6; Mismatches 8;
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Claim 1; Fig 4; 144pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90.9%;
90.1%;
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Best Local Similarity 90.1
Matches 128; Conservative
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The invention relates to a novel chimeric or human monoclonal antibody or its antigen-binding portion that specifically binds to and activates human CD40. The anti-CD40 antibody of the invention demonstrates cytostatic, virucide, antibacterial, immunostimulant and anti-HIV such as cancer, virucide, antibacterial, immunostimulant and anti-HIV such as cancer, viral and bacterial infection or genetic, primary or combined immunodeficiency conditions including neutropenia or HIV infection. The anti-CD40 antibodies may also be useful for detecting CD40 in a biological sample in vitro or in vivo, as well as during gene therapy procedures. The current sequence is that of the human anti-CD40 antibody full length light chain protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 METPAQLLFLLLLWLPDTTGELALTQSPGTLSLSPGERATLSCRASQSFSSSYLAWYQQK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89.8%; Score 658.5; DB 7; Length 234; 90.1%; Pred. No. 4.7e-37; ive 7; Mismatches 6; Indels 1
                                                                                                    Claim 7; SEQ ID NO 88; 177pp; English.
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30-MAR-2001; 2001JP-00099508.
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Matches 128; Conservative
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N-PSDB; AAS99475.
viral infections.
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The invention relates to a novel human antibody (I), preferably a human monoclonal antibody which binds to an activation inducible lymphocyte immunomodulatory molecule (AILIM). (I) is useful for modulating signal transduction into a cell mediated by AILIM, for modulating proliferation of AILIM-expressing cells, for modulating production of a cytokine from AILIM-expressing cells and for inducing antibody-dependent cytotoxicity against AILIM-expressing cells and/or immune cytolysis or apoptosis of AILIM-expressing cells and/or immune cytolysis or apoptosis of AILIM-expressing cells and/or immune cytolysis or apoptosis of AILIM-expressing cells and/or immune cytolysis or apoptosis of AILIM-expressing cells. (I) is useful for treating and preventing various diseases associated with AILIM-mediated costimulatory transduction, and for inhibiting the onset and/or advancement of the cheumatoid arthritis, multiple sclerosis, autoimmune thyroiditis, allergic contact-type dermatitis, chronic inflammatory dermatosis, serious errhematosus, insulin-dependent diabetes mellitus, psoriasis, autoimmune or allergic diseases, immune rejection, disorders of the intestinal disorders such as ulcerative colitis, pneumonia, hepatitis, nephritis, vasculitis, and pancreative colitis, pneumonia, hepatitis, nephritis, vasculitis, and pancreative; (I) induces no serious antipenicity (HAMM) in a host. AAU743301 represent anti-human anti-mouse antigenicity (HAMM) in a host. AAU743301 represent anti-human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PGQAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQKYGTSAI-TF 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 PGQAPGLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQFGSSPMCSF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 METPAQLIFLILIMIPDITGEIVITQSPGTLSISPGERATLSCRASQNIRSSYLAWYQQK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Monoclonal antibody, variable region, heavy chain, light chain, VH; VL; complementarity determining region, CDR; MAb; BO2Cll; conformational epitope, factor VIII; KRIXI, von Willebrand factor; hemostasis, intravascular coagulation, arterial thrombosis; arterial restenosis, venous thrombosis, arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 METPAQLIFILLLWIPDTIGETALTOSPGTLSLSPGERATLSCRASQSFSSSYLAWYQQK
             New human monoclonal antibody that binds to activation inducible lymphocyte immunomodulatory molecule, useful for treating rheumatoid arthritis, multiple sclerosis and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89.8%; Score 658.5; DB 5; Length 236;
89.5%; Pred. No. 4.7e-37;
live 8; Mismatches 6; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Light chain variable region VL of KRIX1.
                                                                                                      Claim 30; Page 284-285; 300pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 GOGTRLEIKGTVAAPSVFIFPPS 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 GQGTKLEIKRTVAAPSVFIFPPS 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB47061 standard, protein, 143 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43. .54
/label= CDR1
69. .75
/label= CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 89.5
Matches 128; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 236 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB47061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
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Domain
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complementarity determining region; antibacterial; antiinflammatory
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGTKVEIKRTVAAPSVFIFPPS 143
                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure, Fig 13, 41pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY93704 standard; protein; 233
                                                                                                                                                                                                                                                                                                                         ö
                                                                                                          69. .75
/label= CDR2
108. .117
/label= CDR3
                                                                                                                                                                                                                                                          11-JAN-2002; 2002EP-00447005.
                                                                                                                                                                                                                                                                                                                         (COLL-) COLLEN RES FOUND VZW
                                                                                             CDR1
                                                                                                                                                                                                                                                                                          11-JAN-2001; 2001US-0261405P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                 43. .54
/label= (
                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-610270/66.
N-PSDB; AAL49257.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
es 128; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 143 AA;
                                                                                                                                                                                                                                                                                                                                                        Jacquemin MG,
                                                                                                                                                                                           EP1222929-A2
                                  Homo sapiens
                                                                                                                                                                                                                            17-JUL-2002.
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                                                                               Region
                                                                                                                                               Region
                                                                                                              Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ij
                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents the light chain variable region of the monoclonal antibody (MAb), KRIXI. This MAb produced by the call line of the invention, specifically recognises the wild type factor VIII light chain. KRIXI can be used to inhibit the binding of factor VIII light willebrand factor in a dose dependant manner. The new call line KXIXI, is deposited with the Belgian Coordinated Collections of Micro-organisms, under accession number LMBP 5089CB. KRIXI, or fragments of it, optionally with a thrombolytic agent, are useful for the treatment and/or prevention of hemostasis, coagulation disorder or thrombocit pathologic condition such as intravascular coagulation, arterial thrombosis, venous thrombosis or arteriosclerosis, and attentation of coagulation in a mammal. An effective and safe antithrombotic therapy is provided which reduces the risk of bleeding in mammals, more particularly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PGQAPRLLIYGASTRATGIPDRFSGSGSTDFTLTISRLEPEDFAVYYCQKYGTSA-ITF 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PGQAPRLLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDPAVYCQQYGTSALLF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, antibody, B02C11, KRIX1, light chain, heavy chain, inflammation, variable region, factor VIII inhibitor; sepsis, septic shock, thrombus formation, systemic inflammatory response syndrome; CDR, disseminated intravascular coagulation, haemophilia A, immunosuppressive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 METPAQLIFILLIMIPDITGEIALTQSPGTLSLSPGERATLSCRASQSFSSSYLAWYQQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                        Novel cell lines for producing monoclonal antibodies that bind to factor involved in hemostasis and coagulation cascade, useful for treating and preventing coagulation disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 654.5; DB 4;
Pred. No. 5.7e-37;
7; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human KRIX1 light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GOGTRLEIKGTVAAPSVFIFPPS 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ą.
                                                                                                                                                                                                                                                                                                                                                                        Example 5; Fig 9; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAO18879 standard; protein; 143
                                                                                                                                             99GB-00016450.
99US-0143891P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89.3%;
89.5%;
                                                                                                              13-JUL-2000; 2000WO-EP006677
                                                                                                                                                                                          (LEUV-) LEUVEN RES & DEV VZW
                                                                                                                                                                                                                            Saint-Remy JR
 109. .118
/label= CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 89.5
Matches 128, Conservative
                                                                                                                                                                                                                                                          WPI; 2001-138333/14.
N-PSDB; AAC85454.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 143 AA;
                                                WO200104269-A1
                                                                                                                                                                                                                            Jacquemin MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-NOV-2002
                                                                                                                                             14-JUL-1999;
14-JUL-1999;
                                                                               18-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA018879;
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   Domain
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The present invention relates to a pharmaceutical composition for the prevention and/or treatment of systemic inflammatory response syndrome (SIRS), sepsies spock, thrombus formation in the microvasculature and disseminated intravascular coagulation in mammals, comprising as an active ingredient a partial inhibitor of factor VIII, in admixture with a carrier. Such inhibitors may include the antibodies B02011 and KRIXI. The present sequence is the light chain variable region of KRIXI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PGQAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQKYGTSA-ITF 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 METPAQLIFILILIMUPDTTGEIVITQPPGTLSLSPGERATLSCRASQSVASAXTAWYQQK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system; hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 METPAQLLFLLLLWLPDTTGEIALTQSPGTLSLSPGERATLSCRASQSFSSSYLAWYQQK
Pharmaceutical composition for treating systemic inflammatory respons syndrome, sepsis, septic shock and/or thrombus formation in microvasculature in mammals, comprises a partial inhibitor of factor VIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89.3%; Score 654.5; DB 5;
89.5%; Pred. No. 5.7e-37;
ive 7; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The kappa chain of immunoglobulin clone 4.8.1.
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Location/Qualifiers

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                                                                                                                                                                                                                                                                                        The present sequence represents a kappa chain of an antibody of the invention. The antibody is directed cytotoxic T-lymphocyte antibody -4. Antibodies of the invention are composed of a heavy chain variable region, comprising a modified contiguous sequence from a FRI-FR3 sequence encoded by a human VRB-33 family gene. The modifications are contained in CDR1, CDR2 and/or framework regions. The antibodies may be used to inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity disorders (e.g. autoimmune disease, diabetes and graft rejection) and proliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be used to up-regulate immune system to up-regulate immune system to up-regulate immunodeficient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 PGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGISPFTFG 118
                                                                                                                                                                                                                             (CTIA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system; hyperimmunity disorder; autoimmune disease; diabetes; graft rejection; proliferative disorder; cancer; immunodeficient disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 METPAQILIFILLIMLPDTTGEIVLTQSPGTLSLSPGERATLSCRT--SVSSSYLAWYQQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PGQAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQKYGTSAITFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 METPAQLLFLLLLWLPDTTGEIALTQSPGTLSLSPGERATLSCRASQSFSSSYLAWYQQK
                                                                                                                                                             Davis CG;
                                                                                                                                                                                                                         Novel antibodies capable of binding cytotoxic T-lymphocyte antigen -4 containing specified heavy and light chain sequences, useful for treating, e.g. immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5
                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 654; DB 3; Length 233; Pred. No. 9.4e-37; Aismatches 8; Indels
                                                                                                                                                            Gilman SC,
proliferative disorder; cancer; immunodeficient disorder.
                                                                                                                                                            Mueller EE, Hanke JH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The kappa chain of immunoglobulin clone 4.8.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QGTRLEIKGTVAAPSVFIFPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGTKVEIKRTVAAPSVFIFPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY93731 standard; protein; 233
                                                                                                                                                                                                                                                                      Claim 3; Fig 1B; 157pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                              89.2%;
90.1%;
                                                                                     99WO-US030895.
                                                                                                        98US-0113647P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                             Neveu MJ,
                                                                                                                                                                                             2000-442647/38.
                                                                                                                                       ABGENIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                      N-PSDB; AAA46867
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 233 AA;
                                                                                                                            (PFIZ ) PFIZER (ABGE-) ABGENIX
                                           WO200037504-A2
                     Homo sapiens.
                                                                                     23-DEC-1999;
                                                                                                         23-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-OCT-2000
                                                                                                                                                                      Corvalan JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Simi
Matches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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The present sequence represents a kappa chain of an antibody of the invention. The antibody is directed cytocoxic T-lymphocyte antipagen (CTLA) 4. Antibodies of the invention are composed of a heavy chain variable region, comprising a modified contiguous sequence from a FRI-FR3 sequence encoded by a human VRI-331 family gene. The modifications are contained in CDR1, CDR2 and/or framework regions. The antibodies may be used to inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity proliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be used to yeel framework regions to the system to treat hyperimmunity proliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be used to up-regulate immune system to up-regulate immunodeficient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel antibodies capable of binding cytotoxic T-lymphocyte antigen (CTLA) -4 containing specified heavy and light chain sequences, useful for treating, e.g. immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PGQAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQKYGTSAITFG
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                                                                                                                                                                                                                                                                                                                                                                                          Davis CG;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 654; DB 3; Length 23
Pred. No. 9.4e-37;
1; Mismatches . 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human 4.8.1 anti-CTLA-4 antibody kappa chain.
                   1. .20
/note= "signal peptide"
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                                                                                                                                                                                                                                                                                                                                                                                          Mueller EE,
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90.1%;
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                                                                                                                                                                                                                                                                                                                                                                                             Neveu MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-442647/38.
                                                                                                                                                                                                                                                                                                              (PFIZ ) PFIZER INC. (ABGE-) ABGENIX INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAA46895.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 233 AA;
                                                                                                                                                                                                                                                                                                           (PFIZ ) PFIZER
                                                                                                  WO200037504-A2
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                                                                                                                                                                                                        23-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                          Hanson DC, 1
Corvalan JR;
                                                                                                                                                     29-JUN-2000
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Key
Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
AAE35886
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antiallergic; antiulcer; neuroprotective; antithyroid; vasotropic; immunosuppressive; dermatological; antiinflammatory; hepatotropic; activation inducible lymphocyte immunomodulatory molecule; ALLIN monoclonal antibody; allergy; rheumatoid arthritis; diabetes mellitus; multiple sclerosis; autoimmune thyroiditis; psoriasis; hepatitis; allergic contact-type dermatitis; ohronic inflammatory dermatosis; systemic lupus erythematosus; autoimmune disorder; inflammation; graft versus host reaction; immune rejection; intestinal immunity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 METPAQLEFILLLMIPPTTGEIVLTQSPGTLSLSSPGERATLSCRT--SVSSSYLAWYQQK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59 PGQAPKLLIYGASSRATGIPDRFSGSGSGTDFTLTISKLEPEDFAVYVCQQYGISPFTFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 METPAQLIFILLIMIPDITGEIALIQSPGTLSLSPGERATLSCRASQSFSSSYLAWYQQK
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                                                                                                                                                                                                                                                                                                                                                                                       Use of human anti-cytotoxic T lymphocyte antigen-4 antibody in the preparation of medicament for the treatment of cancer.
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                                                                                     /note= "Mature anti-CTLA-4 antibody kappa chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 89.2%; Score 654; DB 6; Length 233; Local Similarity 90.1%; Pred. No. 9.4e-37; Les 128; Conservative 4; Mismatches 8; Indels
                                1. .20
/label= Signal peptide
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               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure, Fig 1K; 76pp; English.
                                                                                                                                                                                                                             23-MAY-2001; 2001US-0293042P
                                                                                                                                                                                             23-MAY-2002; 2002EP-00253652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                               (PFIZ ) PFIZER PROD INC
                                                                                                                                                                                                                                                                                                                                     WPI; 2003-131215/13.
N-PSDB; AAD54346.
                                                                                                                                                                                                                                                                                                   Mueller
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                                                                                                                       EP1262193-A1
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                                                                                                                                                         04-DEC-2002
                                                                                                                                                                                                                                                                                                     Hanson DC,
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                              Peptide
                                                                    Protein
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Matches
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임
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The invention relates to a novel human antibody (I), preferably a human monoclonal antibody which binds to an activation inducible lymphocyte immunomodulatory molecule (AILIM). (I) is useful for modulating signal transduction into a cell mediated by AILIM, for modulating proliferation of AILIM-expressing cells, for modulating production of a cytokine from AILIM-expressing cells, and for inducing antibody-dependent cytotoxicity against AILIM-expressing cells and/or immune cytolysis or apoptosis of AILIM-expressing cells and/or immune cytolysis or apoptosis of AILIM-expressing cells. (I) is useful for treating or prophylaxis of delayed type allergy. (I) is useful for treating or prophylaxis of delayed type allergy. (I) is useful for treating or prophylaxis of delayed type allergy. (I) is useful for treating or the prophylaxis of delayed type allergy. (I) is useful for treating or the prophylaxis of allergy the onset and/or advancement of the cheumatoid arthitis, multiple sclerosis, autoimmune thyroiditis, allergic contact-type dermatitis, chronic inflammatory dermatosis, systemic lugue erythematosus, insulin-dependent diabetes mellitus, psoriasis, autoimmune or allergic disorders, inflammatory dermatosis, psoriasis, autoimmune or allergic disorders, inflammatory dermatosis, obst reaction, graft versus host disease, immune rejection, graft versus host disease, immune rejection, graft versus host disease, inmune rejection, contact versus host disease, inmune rejection, contact versus host disease, inmune rejection disorders cansed by abnormal intestinal immunity, specifically inflammatory intestinal disorders such as ulcerative collitis, pneumonia, hepatitis, intestinal disorders such as ulcerative collitis, pneumonia, hepatitis, and pancreative collitis, pneumonia, hepatitis, and pancreaticis. (I) induces no serious anticenting delayed. (I) in a host. AAU142301 represent anti-human anti-human anticon mention anticon and sequences of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New human monoclonal antibody that binds to activation inducible lymphocyte immunomodulatory molecule, useful for treating rheumatoid arthritis, multiple sclerosis and inflammation.
ulcerative colitis; pneumonia; nephritis; vasculitis; pancreatitis.
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89.5%; Pred. No. 1e-36;
iive 8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 30; Page 298-299; 300pp; English.
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                                                                                                                                                                                                   15-MAY-2001; 2001WO-JP004035
                                                                                                                                                                                                                                                18-MAY-2000; 2000JP-00147116
30-MAR-2001; 2001JP-00099508
                                                                                                                                                                                                                                                                                                                                                                           Hori N;
                                                                                                                                                                                                                                                                                                                              (NISB ) JAPAN TOBACCO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 89.5
Matches 128; Conservative
                                                                                                                                                                                                                                                                                                                                                                           Tsuji T, Tezuka K,
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N-PSDB; AAS99477.
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                                                                                                  WO200187981-A2
                                                     Homo sapiens.
                                                                                                                                                     22-NOV-2001
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AAY93733
ID AAY93
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AAY93733;

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4. Antibodies of the invention are composed of a heavy chain variable region, comprising a modified contiguous sequence from a FRI-FR3 sequence encoded by a human VH3-33 family gene. The modifications are contained in CDR1, CDR2 and/or framework regions. The antibodies may be used to inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity disorders (e.g. cancer). CTLA-4 stimulatory agents and proliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be used to used to up-regulate immune system to up-regulate immune system to up-regulate immunodeficient
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PGOAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQKYGTSAITFG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel antibodies capable of binding cytotoxic T-lymphocyte antigen (CTLA) -4 containing specified heavy and light chain sequences, useful for treating, e.g. immune disorders.
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                                                                                            Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system; hyperimmunity disorder; autoimmune disease; diabetes; graft rejection; proliferative disorder; cancer; immunodeficient disorder.
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                                                                 The kappa chain of immunoglobulin clone 6.1.1.
                                                                                                                                                                                                                      1. .20
/note= "signal peptide"
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                                                                                                                                                                                                      Location/Qualifiers
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                                03-OCT-2000 (first entry)
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N-PSDB; AAA46897.
                                                                                                                                                                                                                                                                                                                                                                                                           (PFIZ ) PFIZER INC. (ABGE-) ABGENIX INC
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Corvalan JR;
                                                                                                                                                                         Homo sapiens
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Search completed: April Job time: 46.8917 secs

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Sequence 4, Appli
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733
1 METPAQLLFLLLLMLPDTTG.....TRLBIKGTVAAPSVFIFPPS 142
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1: /cgm2_6/prodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgm2_6/prodata/2/pubpaa/PCT_NEW PUB.pep:*
3: /cgm2_6/prodata/2/pubpaa/US06_NEW PUB.pep:*
4: /cgm2_6/prodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgm2_6/prodata/2/pubpaa/US06_PUBCOMB.pep:*
6: /cgm2_6/prodata/2/pubpaa/US08_NEW PUB.pep:*
7/cgm2_6/prodata/2/pubpaa/US08_NEW PUB.pep:*
8: /cgm2_6/prodata/2/pubpaa/US08_NEW PUB.pep:*
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11: /cgm2_6/prodata/2/pubpaa/US09E_PUBCOMB.pep:*
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12: /cgm2_6/prodata/2/pubpaa/US09E_PUBCOMB.pep:*
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14: /cgm2_6/prodata/2/pubpaa/US10A_PUBCOMB.pep:*
15: /cgm2_6/prodata/2/pubpaa/US10A_PUBCOMB.pep:*
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19: /cgm2_6/prodata/2/pubpaa/US10A_PUBCOMB.pep:*
11: /cgm2_6/prodata/2/pubpaa/US10A_PUBCOMB.pep:*
18: /cgm2_6/prodata/2/pubpaa/US10A_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-044-569B-8

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US-09-782-397-5

US-10-309-764-89

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US-10-153-382-7
US-10-180-648-4
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                              - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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807	4,	4	7	91,	93,	122	332	334	50,	86,	80,	107	107		42,						4,	4,	72,	38,	44,	76,	78,			
equenci	ednenci	Seguence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sednence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Seguence	Seguence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	
-10-291-265-	9-848-832	-10-225-108A	-10-461-148-2	-10-309-762-9	-10-309-762-9	-10-307-724-12	-10-291-265-3	0-291-265-3	-09-453-234-5	-09-453-234-8	-09-453-234-8	-10-216-484-10	-10-384-933-10	-09-972-656-1	-09-453-234-4	-10-216-484-	-10-384-933-5	-09-453-234-7	-10 - 153 - 38	-453-234-5	-10-226-615-	-10-374-93	-09-453-234-7	-453-234-3	-09-453-234-4	-453-234-7	-09-453-234-7	-09-453-234-40	-764-1	
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ALIGNMENTS

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US-10-044-569B-4

JOEGALOW 1920030175268A1

Sequence 4, Application US/10044569B

Publication No. US20030175268A1

Sequence 4, Application US/20030175268A1

SERVEAL INTORMATION:

APPLICANT: D. Collen Research Foundation vzw

APPLICANT: Jacquenin, Marc G

APPLICANT: Saint-Remy, Jean-Marie R

TITLE OF INVENTION: And/or treating systemic inflammatory response syndrome FILE REPRENCE: C1968

TITLE OF INVENTION: And/or treating systemic inflammatory response syndrome FILE REPRENCE: C1060

TITLE OF INVENTION WUMBER: US/02-01-11

PRIOR PILING DATE: 2001-01-11

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PARCHE 2001-01-11

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PARCHE: C162

NUMBER OF SEQ ID NOS: 4

SEQ ID NO 4

LENTH: 142

TYPE: PRI
ORGANISM: Homo sapiens

FRAUNE: NAME/KEY: misc_feature

LOCATION: (205). ..(351)

OTHER INFORMATION: complementary determining region number two FRAUNE:

NAME/KEY: misc_feature

LOCATION: (205). ..(351)

OTHER INFORMATION: complementary determining region number two FRAUNE:

NAME/KEY: misc_feature

LOCATION: (205). ..(351)

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NAME/KEY: misc_feature

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NAME/KEY: misc_feature

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NAME/KEY: misc_feature

LOCATION: (205). ..(351)

OTHER INFORMATION: complementary determining region number two FRAUNE:

NAME/KEY: misc_feature

LOCATION: (205). ..(351)

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NAME/KEY: misc_feature

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NAME/KEY: misc_feature

LOCATION: (325). ..(351)

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NAME/KEY: misc_feature

LOCATION: (325). ..(351)

OTHER INFORMATION: complementary determining region number one FRAUNE:

NAME/KEY: misc_feature

LOCATION: (325). ..(351)

OTHER INFORMATION: com
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Query Match
Best Local Similarity 90.1
Matches 128; Conservative
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; ORGANISM: Homo sapiens
US-09-859-053-34
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US-10-044-569B-8
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                                                                             PGQAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQKYGTSAITFG 120
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93.0%; Score 682; DB 14; Length 235;
Best Local Similarity 92.3%; Pred. No. 1.1e-50;
Matches 131; Conservative 6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                Sequence 7, Application US/10153382
Publication No US20030086930A1
GENERAL INFORMATION:
APPLICANT: PFIZER PRODUCTS INC.
TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
FILE REPRENCE: PC2019A
CURRENT APPLICATION NUMBER: US/10/153,382
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: 60/293042
PRIOR FILING DATE: 2001-05-23
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/10180648
Publication No. US2004003353A1
GENERAL INFORMATION:
APPLICANT: Boyle, William J
APPLICANT: Corvalan, Jose R
APPLICANT: Corvalan, Jose R
APPLICANT: Corvalan, Jose R
APPLICANT: Davis, C. Geoffrey
TILE OP INVENTION: Antibodies to OPGI.
FILE REFERENCE: 06843.0049-00000
CURRENT APPLICATION NUMBER: US/10/180,648
CURRENT FILING DATE: 2001-0-25
PRIOR APPLICATION NUMBER: 60/301,172
PRIOR FILING DATE: 2001-06-26
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PATENTIN Version 3.1
SEQ ID NO 4
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// ORGANISM: Mus musculus
US-10-180-648-4
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US-10-153-382-7
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Sequence 8, Application US/10044569B
Publication No. US2003017526841
GENERAL INFORMATION:
APPLICANT: D. Collen Research Foundation vzw
APPLICANT: Jacquenin, Marc G
APPLICANT: Saint-Remy, Jean-Marie R
TITLE OF INVENTION: Method and pharmaceutical composition for preventing
TITLE OF INVENTION: and/or treating systemic inflammatory response syndrome
FILE REPERENCE: C1968
CURRENT APPLICATION NUMBER: US/10/044,569B
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APPLICANT: TBUJI, Takashi
APPLICANT: TBUJI, Takashi
APPLICANT: TEUJA, KATSUNATI
APPLICANT: TEZUKA, KATSUNATI
APPLICANT: HUMAN (NOCLONAL ANTEDDY AGAINST A
TITLE OF INVENTION: HUMAN MONOCLONAL ANTEDDY AGAINST A
TITLE OF INVENTION: PHARVACEUTICAL USE THEREOF
TITLE OF INVENTION: PHARVACEUTICAL USE THEREOF
TITLE OF INVENTION: PHARVACEUTICAL USE THEREOF
TITLE OF INVENTION: PHARVACEUTICAL USE THEREOF
TITLE OF INVENTION NUMBER: US/09/859,053
CURRENT APPLICATION NUMBER: JP 2001-99508
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2000-05-18
NUMBER: OF SEQ ID NOS: 43
                                                                                                                                                        1 METPAQILFLILLMLPDTTGEIVLTQSPGTLSLSPGERATLSCRASQSVRGRYLAWYQQK
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Length 235;
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                                                         Indels
Score 666; DB 12;
Pred. No. 2.7e-49;
6; Mismatches 8;
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Pred. No. 1.2e-48;
8; Mismatches 6
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      90.08;
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Best Local Similarity 89.5%;
Matches 128; Conservative
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119 GGTKVEIKRTVAAPSVFIFPPS 140
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NAME/KEY: misc feature
LOCATION: (1255)..(354)
CHER INFORMATION: complementary determining region number three
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89.3%; Score 654.5; DB 14; Length 143;
Best Local Similarity 89.5%; Pred. No. 1.5e-48;
Matches 128; Conservative 7; Mismatches 7; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: (127)..(162)
OTHER INFORMATION: complementary determining region number one
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LOCATION: (205)..(225)
OTHER INFORMATION: complementary determining region number
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| Sequence 11, Application US/10153382
| Publication No. US20030086930A1
| GENERAL INFORMATION:
| APPLICAM' PFIZER PRODUCTS INC.
| TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
| FILE PEPERANCE:
| CURRENT APPLICATION NUMBER: US/10/153,382
| CURRENT FILING DATE: 2002-05-22
| PRIOR APPLICATION NUMBER: 60/293042
| PRIOR FILING DATE: 2001-05-23
| NUMBER OF SEQ ID NOS: 39
| SEQ ID NOS: 39
| SEQ ID NO II OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL OF IL 
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Pred. No. 2.8e-48;
4; Mismatches 8;
CURRENT FILING DATE: 2002-01-11
PRIOR APPLICATION NUMBER: US 60/261,405
PRIOR FILING DATE: 2001-01-11
WUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.1
SEQ ID NO 8
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Best Local Similarity 90.1%;
Matches 128; Conservative
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CORGANISM: Homo sapiens
US-10-153-382-11
                                                                                                                                                                                                                                                   LENGTH: 143
TYPE: PRT
ORGANISM: Homo sapiens
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Sequence 38, Application US/09859053
; Sequence 38, Application US/09859053
; Patent No. US20020102658A1
; GENERAL INFORMATION:
    GENERAL INFORMATION:
    APPLICANT: TSUJi, Takashi
    APPLICANT: TSUJi, Takashi
    APPLICANT: TSUJi, Takashi
    APPLICANT: HOWEN WONDOLONAL ANTIBODY AGAINST A
    TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
    TITLE OF INVENTION: HPARMAGEUTICAL USE THEREOF
    TITLE OF INVENTION: HPARMAGEUTICAL USE THEREOF
    TITLE OF INVENTION: HPARMAGEUTICAL USE THEREOF
    TITLE OF INVENTION NUMBER: US/09/859,053
    CURRENT APPLICATION NUMBER: US/09/859,053
    CURRENT FILING DATE: 2001-03-30
    PRIOR FILING DATE: 2001-03-30
    PRIOR FILING DATE: 2000-05-18
    NUMBER OF SEQ ID NOS: 43
    SOFWHARE: FastSEQ for Windows Version 4.0
    LENGTH: 236
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Pred. No. 5.7e-48;
5; Mismatches 9; Indels 1;
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US-10-153-382-15
Sequence 15, Application US/10153382
Publication No. US20030086930A1
GENERAL INFORMATION:
APPLICANT: PPIZER PRODUCTS INC.
TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
FILE REFERENCE: PC23019A
CUTRENT APPLICATION UNMBER: US/10/153,382
CUTRENT APPLICATION NUMBER: 05/293042
PRIOR APPLICATION NUMBER: 60/293042
PRIOR FILING DATE: 2001-05-23
PRIOR FILING DATE: 2001-05-23
VUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89.2%; Score 653.5; DB 9 89.5%; Pred. No. 3.2e-48; iive 8; Mismatches 6
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Best Local Similarity 89.4%;
Matches 127; Conservative
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Best Local Similarity 89.5'
Matches 128; Conservative
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CORGANISM: Homo sapiens
US-10-153-382-15
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; ORGANISM: Homo sapiens
US-09-859-053-38
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LENGTH: 234
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ION: (80)
INFORMATION: Xaa equals any of the naturally occurring L-amino acids
KEY: SITE
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THER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ION: (3) INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       equals any of the naturally occurring L-amino acids
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INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      equals any of the naturally occurring L-amino acids
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81.9%; Score 600.5; DB 11; Length 236;
Best Local Similarity 84.7%; Pred. No. 1.1e-43;
Matches 122; Conservative 3; Mismatches 16; Indels 3;
                                                                                                                                                                                         Sequence 237, Application US/09833245
Publicalion No. US20040010134A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF546PCT
CURRENT APPLICATION NUMBER: US/09/833,245
CURRENT APPLICATION NUMBER: 60/229, 358
PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR FILING DATE: 2000-04-12
PRIOR PILING DATE: 2000-04-12
PRIOR PILING DATE: 2000-04-12
PRIOR PILING DATE: 2000-04-12
PRIOR PILING DATE: 2000-04-12
NUMBER OF SEQ 1D NOS: 2267
NUMBER OF SEQ 1D NOS: 2267
125 ITFGGGTKVBIKRTVAAPSVFIFPPS 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FGXGTKVEIKRTVAAPSVFIFPPS 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (29)
OTHER INFORMATION: Xaa
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION: Xaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ION: (97)
INFORMATION: Xaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 237
LENGTH: 236
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-Publication No. US20030021779A1
-GENERAL INFORMATION:
APPLICANT: Dan, Michael D.
Malti, Pradip K.
Kaplan, Howard A.

TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT
SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE
FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
DETECTION OF CANCERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 PGQAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQKYGTS---A 116
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          METPAQLLFLLLLUMLPDTTGEIVLTQSPGTLSLSPGERATLSCRASQSV-SSYLAWYQQK 59
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MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster LLP
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 ITFGQGTRLEIKGTVAAPSVFIFPPS 142
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                                                                                                                                                                                                                                          120 PGTKVDIKRTVAAPSVFIFPPS 141
                                                                                                                                                                                                   121 OGTRLEIKGTVAAPSVFIFPPS 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (650) 494-0792
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SEQUENCE CHARACTERISTICS
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Best Local Simi
Matches 128;
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us-10-044-569b-4.rapb

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Sequence 805, Application US/10291265

publication No. US20030232054A1

GENERAL INFORMATION:

APPLICANT: Hyseq, Inc.

APPLICANT: Tang et al.

TITLE OF INVENTION: US.

CURRENT APPLICATION NUMBER: US/10/291,265

CURRENT APPLICATION NUMBER: US/10/291,265

PRIOR PILING DATE: 2000-01-25

PRIOR FILING DATE: 2000-01-25

PRIOR FILING DATE: 2000-01-05

PRIOR FILING DATE: 2000-01-05

PRIOR PILING DATE: 2000-01-17

PRIOR PILING DATE: 2000-01-17

PRIOR PILING DATE: 2000-09-17

PRIOR PILING DATE: 2000-09-15

PRIOR PILING DATE: 2000-09-15
                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 804, Application US/10291265; Publication No. US20030232054A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) ORGANISM: Homo sapiens
US-10-291-265-804
                                                                                                                                                                121 QGTRLEIK 128
                                                                                                                                                                                                           ||::|||
|20 GGTKVEIK 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               138 IFPPS 142
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US-10-291-265-805
                                                                                                                                                                                                                                                                                                                                                    RESULT 13
US-10-291-265-804
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US-10-309-764-89

1 Sequence 89, Application US/10309764

2 Publicaction No. US20030232009A1

3 Publicant: NOCMATION:
APPLICANT: Foltz, Ian
APPLICANT: Palathumpat, Raju
APPLICANT: Palathumpat, Raju
APPLICANT: Palathumpat, Raju
APPLICANT: Palathumpat, Raju
APPLICANT: Palathumpat, Raju
APPLICANT: Yang, Chadwick T.
TITLE OF INVENTION: TREATING AUTOIMMUNE DISEASE AND TRANSPLANT REJECTION
TITLE OF INVENTION: TREATING AUTOIMMUNE DISEASE AND TRANSPLANT REJECTION
TITLE OF INVENTION: TREATING AUTOIMMUNE DISEASE AND TRANSPLANT REJECTION
TITLE OF INVENTION: 1202-12-02
PRIOR APPLICATION NUMBER: 60/337,276
PRIOR APPLICATION NUMBER: 60/337,276
PRIOR APPLICATION NUMBER: 60/337,276
PRIOR APPLICATION NUMBER: 60/337,276

PRIOR PILMG DATE: 2001-12-03

NUMBER OF SEC ID NOS: 147

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 89

LENGTH: 128

TYPE: PRT

CREANISM: Home sapiens
US-10-309-764-89
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| Sequence 55, Application US/10309762
| Publication No. US20040018198A1
| GENERAL INFORMATION:
| APPLICANT: Gudae, Jean
| APPLICANT: Handa, Masahisa
| APPLICANT: Handa, Masahisa
| APPLICANT: Handa, Masahisa
| APPLICANT: Goltz, Ian
| APPLICANT: Handa, Masahisa
| APPLICANT: Handa, Masahisa
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81.3%; Score 596; DB 15; Length 128;
Best Local Similarity 89.1%; Pred. No. 1.4e-43;
Matches 114; Conservative 8; Mismatches 6; Indels
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CORGANISM: Homo sapiens
US-10-309-762-95
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|21 GGTKVEIK 128
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APPLICANT: Hyseq, inc.
APPLICANT: Hyseq, inc.
APPLICANT: Tang et al
TITLE OF INVENTION: No. US20030232054Alel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-017 (785)
CURRENT APPLICATION NUMBER: US/10/291,265
CURRENT APPLICATION NUMBER: 09/491,404
PRIOR PILING DATE: 2000-01-25
PRIOR PILING DATE: 2000-01-25
PRIOR PILING DATE: 2000-07-17
PRIOR APPLICATION NUMBER: 09/631,451
PRIOR PILING DATE: 2000-07-17
PRIOR APPLICATION NUMBER: 09/631,451
PRIOR PILING DATE: 2000-09-15
PRIOR FILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 944
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              227 GIPDRESGSGGTDFTLATISRLEPEDFAVYYCQQYGSSPTTFGQGTKVDIKRTVAAPSVF 286
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61 PGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPDDFAVYCQHYGRS-LTFG 119
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80.5%; Score 590; DB 15; Length 384;
Best Local Similarity 90.4%; Pred. No. 1.4e-42;
Matches 113; Conservative 7; Mismatches 5; Indels C
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publication No. US20030232054A1

publication No. US20030232054A1

GENERAL INFORMATION:

APPLICANT: Hyseq, Inc.

APPLICANT: Hyseq, Inc.

APPLICANT: Tang et al.

TITLE OF INVENTION: No. US20030232054A1e1 Nucleic Acids and Polypeptides

FILE REFERENCE: 21272-017 (785)

CURRENT APPLICATION NUMBER: US/10/291,265

CURRENT FILING DATE: 2000-01-25

PRIOR FILING DATE: 2000-01-25

PRIOR FILING DATE: 2000-01-3

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-09-15

NUMBER OF SEQ ID NOS: 944

SOFFWARE: FastSEQ for Windows Version 3.0
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80.5%; Score 590; DB 15; Length 384;
Best Local Similarity 90.4%; Pred. No. 1.4e-42;
Matches 113; Conservative 7; Mismatches 5; Indels (
                                                                                                                                                                          Length 384;
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80.5%; Score 590; DB 15;
Best Local Similarity 90.4%; Pred. No. 1.4e-42;
Matches 113; Conservative 7; Mismatches 5;
; NUMBER OF SEQ ID NOS: 944
; SOFWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 805
; LENGTH: 384
; TYPE: PRT
; ORGANISM: HOMO sapiens
US-10-291-265-805
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CRGANISM: Homo sapiens
US-10-291-265-806
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-US-WILL CLOCK THE APPLICATION US/09472087

Patent No. 668736

GENERAL INFORMATION:

APPLICANT: HANSON, DOUGLAS C.
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: HANSON, BILEN E.

APPLICANT: HANSON, SIEVEN C.
APPLICANT: HANSON, GEOFFREY

APPLICANT: HANSON, GEOFFREY

APPLICANT: CORVALAN, JOSE R.

TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4

FILE REFERENCE: ABX-PPI

CURRENT APPLICATION NUMBER: US/09/472,087

CURRENT FILICATION NUMBER: 06/113,647

PRIOR PLICATION NUMBER: 06/113,647

RIOR PLICATION NUMBER: 06/113,647

RIOR PLICATION NUMBER: 06/113,647

ROUGHAND BATE: 1999-12-23

NUMBER OF SEQ ID NOS: 147

SEQ ID NO 14

LENGTHREES
US-08-812-586-16
US-09-535-822A-17
US-08-276-823-832A-17
US-08-899-575-153
US-08-899-577-153
US-09-472-087-21
US-09-472-087-21
US-09-472-087-93
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US-09-472-087-65
US-09-472-087-65
Sequence 65, Application US/09472087
Patent No. 6682736
GENERAL INPORMATION
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: NEVEU, MARK J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-14
        Query Match
Best Local Simil
Matches 131, C
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575.678 Million cell updates/sec
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// cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-402-124-6
US-08-402-134-4
US-08-402-134-4
US-08-402-131-183
US-08-053-131-183
US-09-042-333-46
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61 PGQAPRILLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQKYGTSAITFG 120
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APPLICANT: HANKE, JEFREK H.
APPLICANT: HANKE, JEFREK H.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: DAVIS, C. GEOFFREY
APPLICANT: DAVIS, C. GEOFFREY
APPLICANT: OSCYALAN, JOSE R.
TITLE OF INVENTION: HUMAN MONCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABX-PF1
CURRENT APPLICATION NUMBER: 05/94/72,087
CURRENT FILING DATE: 1999-12-23
PRIOR PILING DATE: 1999-12-23
PRIOR FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 147
SOFFWARE: PATENTIN Ver. 2.1
SEQ ID NO 67
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APPLICANT: CORVALAN, JOSE R.
APPLICANT: CORVALAN, JOSE R.
APPLICANTON: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABX-PF1
CURRENT PAPPLICATION NUMBER: US/09/472,087
CURRENT FILING DATE: 1999-12-23
PRIOR PRICATION NUMBER: 60/113,647
PRIOR PLING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PATENTIN Ver. 2.1
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Pred. No. 4.1e-52;
4; Mismatches 8;
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     121 QGTRLEIKGTVAAPSVFIFPPS 142
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Patent No. 6682736
GENERAL INFORMATION:
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: NEVEU, MARK J.
                                                                                                                                                                        Sequence 67, Application US/09472087
Patent No. 6682736
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HANKE, JEFFREY H.
GILMAN, STEVEN C.
DAVIS, C. GEOFFREY
CORVALAN, JOSE R.
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90.1%;
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APPLICANT: HANSON, DOUGLAS C.
APPLICANT: NEVEU, MARK J.
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Best Local Similarity 90.1
Matches 128; Conservative
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CORGANISM: Homo sapiens
US-09-472-087-67
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LENGTH: 234
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APPLICANT: HANKE, JEFFREY H.
APPLICANT: HANKE, JEFFREY H.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: OAVIS, C. GEOFFREY
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILLE REFRENCE: ABX.FF1
CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/113,647
PRIOR APPLICATION NUMBER: 60/113,647
PRIOR APPLICATION NUMBER: 60/113,647
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 147
SOFFWARE: PALENTIN Ver. 2.1
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Pred. No. 4.1e-52;
4; Mismatches 8; Indels
APPLICANT: HANKE, JEFREY H.
APPLICANT: GLIMAN, STEVEN C.
APPLICANT: GLIMAN, STEVEN C.
APPLICANT: DAVIS, C. GEOFFREY
TYPLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 147
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 65
LENGTH: 235
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Pred. No. 1.2e-54;
6; Mismatches 5; Indels
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Patent No. 6682736
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90.1%;
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Best Local Similarity 92.3%;
Matches 131; Conservative
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Best Local Similarity 90.1
Matches 128; Conservative
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CRGANISM: Homo sapiens
US-09-472-087-65
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US-09-472-087-15
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LENGTH: 23
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61 PGQAPRLLIYGASTRATGIPDRPSGSGSGTDFTLTISRLEPEDFAVYYCQKYGTS----A 116
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Fatent No. 5744885

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Patent No. 574486

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Patent No. 57486

Patent No. 574486

Patent No. 574486

Patent No. 574486

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                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/862,124
FLING DATE: 22-MAY-1997
CLASSIPICATION: 424
ATTORNEY FAGENT INFORMATION:
NAME: Lebhhardt, Susan K.
REGISTRATION NUMBER: 31,943
REFERENCE/DOCKET NUMBER: 31608-20001.20
TELERAXINO NUMBER: 31,943
REPERENCE/DOCKET NUMBER: 31600
TELERAXINO FOR 494-0792
TELERAX: (650) 494-0792
TELERAX: 706.44
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 150 amino acids
"VDF. amino acids
"VDF. amino acids
"VDF. amino acids
"VDF. amino acids
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87.7%; Pred. No. 7.1e-52;
tive 6; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 ITFGOGTRLEIKGTVAAPSVFIFPPS 142
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TITLE OF INVENTION: DETECTION OF CANG
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORTISON & FOERSET LLP
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: WISCOUNTRY: USA
COUNTRY: US 21P - 23717-1914
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 87.7
Matches 128; Conservative
                                                                                                                                                                                                                                             ZIP: 94304-1018
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                            61 PGQAPRILLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQKYGTSAITFG 120
                                                                                                                                                                                                                                                                                                                                                                                                                      60 PGQAPRPLIYGVSSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYXCQQYGISPFTFG 119
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                                                                                                                                                                                                                                                                                       1 METPAQLIFILLIWI.PDTTGEIVLTQSPGTLSLSPGERATLSCRASQSV-SSYLAWYQQK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTIGEN BINDING FRAGMENTS H11, THAT SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCOI FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 METPAQLLFLLLLWLPDTTGEIALTQSPGTLSLSPGERATLSCRASQSFSSSYLAWYQQK
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                                                                                    DB 4; Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 69, Application US/09472087

Patent No. 6682736

GENERAL INPORMATION:
APPLICANT: HANSO, DOUGLAS C.
APPLICANT: HANCE, BILEN E.
APPLICANT: GILAN, JEFREY H.
APPLICANT: GILAN, JEFREY H.
APPLICANT: GILAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABX-PPI
CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT APPLICATION NUMBER: US/09/472,087

CURRENT APPLICATION NUMBER: 60/113,647

PRIOR PILING DATE: 1999-12-23

PRIOR FILING DATE: 1999-12-23

NUMBER OF SEQ 1D NOS: 147

SOFTWARE: PATENTIN NOS: 147
                                                                                                                                                     Indels
                                                                            Query Match 88.7%; Score 650.5; DB 4; Best Local Similarity 89.4%; Pred. No. 8.6e-52; Matches 127; Conservative 5; Mismatches 9;
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Patent No. 6207153
GENERAL INFORMATION:
APPLICANT: Maiti, Pradip K.
APPLICANT: Raplan, Howard A.
ITILE OF INVENTION: ANTIGEN BINDIP
ITILE OF INVENTION: FREGMENTS, ANI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 89.4
Matches 127; Conservative
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US-09-472-087-69
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US-09-472-087-69
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TYPE: PRT
               US-09-472-087-17
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COMPUTER READABLE FORM:
MEDIUM TYPE: 1094
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
COMPUTER: BM PC compatible
COMPUTER: BM PC compatible
COMPUTER: BM PC compatible
COMPUTER: BM PC compatible
COMPUTER: BM PC compatible
COMPUTER: BM PC compatible
COMPUTER: BM PC compatible
COMPUTER: 26-ARR-1993
FILING DATE: 26-ARR-1992
ATLING DATE: 16-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
ATTORNEY AGENT INFORMATION:
NAME: SMICK: WILLIAM M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-9-3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 82.1%; Score 602; DB 2; L. Best Local Similarity 90.6%; Pred. No. 1.1e-47; Matches 116; Conservative 4; Mismatches 8;
                   REFERENCE/DOCKET NUMBER: 4145(
TELECOMUTICATION INFORMATION:
TELEPAX: 617-523-3400
TELEFAX: 617-523-3400
TELEFAX: 617-523-6440
TELEFAX: 617-523-6440
TELEFAX: 617-523-6440
TELEFAX: 617-523-6440
TELEFAX: 617-523-6440
TELEFAX: 617-523-6440
SEQUENCE CHARACTERISTICS: LENGTH: 129 anino acids
TYPE: anino acid
TYPE: anino acid
TYPE: anino acid
TYPE: anino acid
TYPE: TOPOLOGY: Illnear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 QGTRLEIK 128
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APPLICANT: MARASCO, Wayne A.
APPLICANT: SOBOSKI, Joseph G.
APPLICANT: SOBOSKI, Joseph G.
APPLICANT: SOBOSKI, Joseph G.
APPLICANT: PASELITUR: William A.
APPLICANT: POSNER, Marshall R.
ITILE OF INVENTION: REACTIVE NEUTRALIZING HUMAN
ITILE OF INVENTION: ANTI-9P 120 RECOMBINANT ANTIBODY, DNA CODING THE SAME
ITILE OF INVENTION: ANTI-9P 120 RECOMBINANT ANTIBODY, DNA CODING THE SAME
ITILE OF INVENTION: ANTI-9P 120 RECOMBINANT ANTIBODY, DNA CODING THE SAME
ITILE OF INVENTION: ANTI-9P 120 RECOMBINANT ANTIBODY, DNA CODING THE SAME
ITILE OF INVENTION: AND USE THEREOF
NUMBER OF SEQUENCES: 16
CONNERS. USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPER EACHS EASTERN: DOS
SUSPTANRE: FASESES OF WINDOWS VERSION 2.0
COMPUTER FASESES OF WINDOWS VERSION 2.0
COMPUTER FASESES OF WINDOWS VERSION 2.0
COMPUTER FASESES OF WINDOWS VERSION 2.0
COMPUTER FASESES OF WINDOWS VERSION 2.0
COMPUTER FASESES OF WINDOWS VERSION 2.0
CHARRENT APPLICATION DATA:
APPLICATION NUMBER: 08-MA-1995
APPLICATION NUMBER: 08-MA-1995
APPLICATION NUMBER: 07/804,652
FILING DATE: 10-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: RESICK, DAVIG S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 PGQAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQKYGTSA-ITF 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 PGQAPSLLIYGASTRATGIPDRFSGSGSGTDFILTISRLEPEDFAVYYCQQYGSSARYTF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 METPAQLIFILILMIPDTIGEIVLIQSPGTISISPGERATISCRASQSFSRSFLAWYQQK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 624.5; DB 1;
Pred. No. 1e-49;
4; Mismatches 6;
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/405,034
                                                                                                CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: SAIA, ChAILES S.
REGIGTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 34656.009
TELECHOMOTICATION INFORMATION:
TELEPHONE: 608-831-2106
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 134 annino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/08480774A Patent No. 5852186 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 91.8%;
Matches 123; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 GOGTRLEIKGTVAA 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein US-08-405-034-4
                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-480-774A-4
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61 PGQAPRILLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQKYGTSAITFG 120
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                                                                                                                                                                                               1 METPAQLLFLLLLWLPDTTGEIVLTQSPGTLSLSAGERATLSCRASQSVSSRYLAWYQQK 60
                                                                                                                                    1 METPAQLIFLILIMIPDITGEIALIQSPGTLSLSPGERATLSCRASQSFSSSYLAWYQQX
                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 183. Application US/08053131
Fatent No. 5661016
GENERAL INFORMATION
THORMATION
TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 200
CITY: San Francisco
STATE: California
                                                                  ;
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Length 129;
                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 METPAQLLFILLIMIPDTTGEIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Squence 183, Application US/08096762

| Saquence 183, Application US/08096762
| Patent No. 5814318
| GENERAL INFORMATION:
| APPLICANT: Lonberg, Nils
| APPLICANT: Kay, Robert M.
| TITLE OF INVENTION: Transgenic No. 5814318-Human Animals for TITLE OF INVENTION: Producing Heterologous Antibodies
| NUMBER OF SEQUENCES: 210
| CORRESPONDENCE ADDRESS: ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 200
| CITY: San Francisco | STRATE: California | COUNTRY: USA
                                                                                                                                                                                                                                                                         Query Match 78.3%; Score 574; DB 1; Length 116; Best Local Similarity 95.7%; Pred. No. 3.4e-45; Matches 110; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CUMULATION OF A 105 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
COMPUTER: ISM PC compatible
COMPUTER: ISM PC compatible
COMPUTER: ISM PC compatible
COMPUTER: ISM PC compatible
SOFTWARE: Percentin Release #1.0, Version #1.25
CUREBNY APPLICATION DATA:
APPLICATION NUMBER: US 08/053,131
FLING DATE: 22-UL-1993
CLASSIFCATION NUMBER: US 07/990,860
FLING APPLICATION NUMBER: US 07/990,860
FLING APPLICATION NUMBER: US 07/990,668
FLING APPLICATION NUMBER: US 07/990,668
FLING APPLICATION NUMBER: US 07/990,068
FLING APPLICATION NUMBER: US 07/991,068
FLING APPLICATION NUMBER: US 07/991,068
FLING APPLICATION NUMBER: US 07/991,068
FLING APPLICATION NUMBER: US 07/991,068
FLING APPLICATION NUMBER: US 07/991,079
FLING APPLICATION NUMBER: US 07/991,079
FLING APPLICATION NUMBER: US 07/991,079
FLING APPLICATION NUMBER: US 07/991,079
FLING APPLICATION NUMBER: US 07/991,079
FLING APPLICATION NUMBER: US 07/991,079
FLING APPLICATION NUMBER: US 07/991,079
FLING APPLICATION NUMBER: US 07/991,079
FLING APPLICATION NUMBER: US 07/991,079
FLING APPLICATION NUMBER: 14643-9-4
TELEPHONE: 415-326-2422
THELEPHONE: 415-326-2422
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 183:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
                                                                                                                                              ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-053-131-183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-096-762-183
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; TYPE: PRT
OGNISM: Homo sapiens
; OTHER INFORMATION: M1-23L
US-09-456-090A-50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 METPAQLIFILLIMLPDTTGEIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 PGQAPRLLIYGASSRATGIPDRPSGSGSGTDPTLTISRLEPEDFAVYYCQQYGSS 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for Producing Heterologous Antibodies
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: San Francisco
CITY: San Francisco
COUNTY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 574; DB 3;
Pred. No. 3.4e-45;
3; Mismatches 2
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APPLICATION NUMBER: US/08/758,417A
FILING DATE: 02-Dec-1996
                  FILING DATE: 09-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US96/16433
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/758,417
FILING DATE: 02-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/758,417
FILING DATE: 02-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/21803
ATTORNEY,AGENT INFORMATION:
US 08/209,741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 311, Application US/08758417A Patent No. 6300129 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 0.14
TELECOMMUNICATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 46: SEQUENCE CHARACTERISTICS: LENGTH: 116 amin ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lonberg, Nils
Kay, Robert M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 95.7%;
Matches 110; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) MOLECULE TYPE: protein US-09-042-353-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-758-417A-311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 METPAQLIFILLIMIPDITGEIALIQSPGTLSLSPGERATLSCRASQSFSSSYLAWYQQX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 PGQAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQKYGTS 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Buechler, Joe
APPLICANT: Buechler, Joe
APPLICANT: Gray, Jeff
APPLICANT: Caray, Jeff
APPLICANT: Londberg, Nils
TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
FILE REFERENCE: 020015-00020005
CURRENT APPLICATION NUMBER: US/09/456,090A
CURRENT FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 110
SOFTWARR: Patentin Ver. 2.1
SSEQ ID NO 50
LENGTH: 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Serafini, Andrew T.
REGIGSTRATION NUMBER: 41,303
REFERENCE/DOCKET NUMBER: 014643-009030US
COMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 78.3%; Score 574; DB 4; Best Local Similarity 95.7%; Pred. No. 3.4e-45; Matches 110; Conservative 3; Mismatches 2
                                                                                                                                 APPLICATION NUMBER: US 08/209/741
APPLICATION NUMBER: US 08/209/741
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/161,739
FILING DATE: 01-DEC-1993
APPLICATION NUMBER: US 08/155,301
APPLICATION NUMBER: US 08/155,301
APPLICATION NUMBER: US 08/155,301
APPLICATION NUMBER: US 08/096,762
                                                   APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
APPLICATION NUMBER: US 08/352,322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 26-APR-1993
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 22-JUL-1993
APPLICATION NUMBER: US 08/053,131
ION NUMBER: US 08/728,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear

NOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 311:
US-08-758-417A-311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 50, Application US/09456090A, Patent No. 6680209, GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (415) 576-
INFORMATION FOR SEQ ID NO: 31
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (415)
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us-10-044-569b-4.rai
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81 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQKYGTS-AITFGQGTRLEIKGTVAAPSVFIF 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 BIALTOSPGTLSLSPGERATLSCRASOSFSSSYLAWYQOKPGQAPRLLIYGASTRATGIP 80
                                                                                                    21 BIALTOSPGTLSLSPGERATLSCRASOSFSSSYLAWYQQKPGQAPRLLIYGASTRATGIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 78.2%; Score 573.5; DB 4; Length 226;
Best Local Similarity 91.9%; Pred. No. 8.2e-45;
Matches 113; Conservative 4; Mismatches 5; Indels 1; Gaps
                                           1; Gaps
                                                                                                                                                                                                                                                                                                                         RESULT 15
US-09-456-090A-86

; Sequence 86, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buchels, Joe
; APPLICANT: Gray, Jeff
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; TITLE OF INVENTION: 199-12-06
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SQTWARE: Patentin Ver. 2.1
; SQ ID NO 86
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Home sapiens
; CTHER INPORMATION: M2-33L
Query Match 78.2%; Score 573.5; DB 4; Length 226; Best Local Similarity 91.9%; Pred. No. 8.2e-45; Matches 113; Conservative 4; Mismatches 5; Indels 1;
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|21 PPS 123
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5, 2004, 13:44:08

Search completed: April Job time : 12.7343 secs

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GenCore version 5.1.6

Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 5, 2004, 13:25:01; Search time 12.6701 Seconds (without alignments)

1184.358 Million cell updates/sec

Title: US-10-044-5693-6

Perfect Acore: 837
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Title: US-10-044-569B-6
Perfect score: 837
Sequence: 1 MDWTWRILFLVAAATGAHSQ......GYTSHYFDYWGRGTLVTVSS 156
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 segs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : PIR 78:*

1: Dirl:*

2: Dir2:*

4: Dir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	anti-Sm antibody V	g heavy cha	chain	g heavy chain V	g heavy	g heavy chain	g heavy	ıti-PR2 erythr	g heavy	g heavy	g heavy chain	g heavy chain	g heavy	g heavy	g heavy chain V	g heavy chain	g mu cha	g heavy	g heavy	g heavy chain	g heavy	g gamma	g heavy	g heavy	g heavy chain	eavy	g heavy chain V	g heavy chain V	Ig heavy chain pre
ai	849530	S23623	S18551	S31600	HVHU35	S31680	831596	PL0105	829257	S19245	846393	D33548	A32483	S18553	S21916	S36265	S14683	HVHUHG	E1HUND	518552	S21924	PT0371	MHMS18	C41287	S18554	HVMST7	869899	PH1669	A30577
DB	2	~	(7	0											N	Ŋ	N	Н	Н	~	N	~	-1	8	~	-	~	ď	N
Length	135	171	Н	ന	Н	_	m	160	ਧਾ	ぜ	N	N	4	-	ന	-	(1	-	4	~	ന	117	(7)	137	4	(,,	104	_	135
* Query Match	72.5	70.7	65.7		65.5		62.5	٠. د		_;	ö	Ċ	ω.	m.	w.	m	œ.	m.	7.	۲.	s.	'n.	'n.	'n.	'n	4	4.	4.	ω.
Score	1 90	591.5	'n	549.5	548	540	523.5	ß	517	515	505	502	498	493	491	490.5	4	486	482.5	477	474	465	Z.	62	460	456	454	53	450.5
Result No.	-	7	М	4	Ŋ	ø	7	00	on	10	11	12	13	14	15	16	17	18	13	20	21	23	23	24	25	26	27	28	29

D.A.; from

Ig heavy chain pre		heavy	heavy	heavy	heavy	heavy	heavy	gamma	heavy	heavy	heavy	Ig heavy chain V r	heavy	Ig gamma-2a chain
E32513	S26938	\$20783	G2MS43	831698	826912	PH1668	F29380	G2MS11	S31667	H32513	S34014	I44151	五29380	537483
010	v (1	N	H	~	~	7	7	Н	N	N	~	N	7	0
138	111	121	137	116	86	109	137	474	116	137	127	126	137	469
53.8	53.4	52.9	52.5	52.4	52.3	52.3	52.3	52.3	52.2	52.0	52.0	51.9	51.8	51.8
450	446	443	439.5	438.5	438	438	437.5	437.5	436.5	435.5	435	434	433.5	433.5
30	32	1 K	34	35	36	37	38	39	40	41	42	43	44	4.5

ALIGNMENTS

RESULT 1 S49530 auti-Sm antibody VH chain (VH1/DK1 or DM1/JH4b) - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 0.1Feb-1995 #sequence_revision 12-May-1995 #text_change 23-Jul-1999 C;Accession: 849530 R;Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D. R;Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D. R;Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D. R;Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D. R;Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D. R;Reference number: 848797 A;Reference number: 848797 A;Residues: preliminary A;Molecule type: mRNA A;Residues: 1-135 < MAH> A;Residues: 1-135 < MAH> A;Cross.references: EMBL:Z46348; NID:g560839; PIDN:CAA86467.1; PID:g560840 E;Superfemily: immunoclobulin V region; immunocloby; Imm	Query Match Best Local Similarity 77.6%; Pred. No. 4.9e-46; Matches 121; Conservative 6; Mismatches 8; Indels 21; Gaps 3; Matches 121; Conservative 6; Mismatches 8; Indels 21; Gaps 3; Qy	RESULT 2 S23623 Ig heavy chain V region precursor - human (fragment) C;Species: Homo sapiens (man) C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999 C;Accession: S23623 R;Olee, T.; Lu, E.W.; Hunng, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, J. Exp. Med. 175, 831-842, 1992 A;Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors A;Reference number: S23623; MUID:92156804; PMID:1740665 A;Accession: S23623 A;Accession: S23623 A;Acseliminary A;Molecule type: DNA A;Residues: 1-171 COLE> A;Cross-references: ENBL:X59702; NID:g32010; PIDN:CAA422223.1; PID:g32011 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Reywords: heterotetramer; immunoglobulin
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Igheavy chain precursor V region (V35) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 21-Jul-2000
C;Accession: 800476; $34013
R;Mateuda, P:; Lee, K.H.; Nakai, S.; Sato, T.; Kodaira, M.; Zong, S.Q.; Ohno, H.; Fukuh
EMBO J. 7, 1047-1051, 1988
A;Title: Dispersed localization of D segments in the human immunoglobulin heavy-chain l
A;Reference number: $00476; MJD:88296408; PMID:2841108
A;Reference number: $00476
A;Molecule type: DNA
A;Residues: 1-17 <AATS>
A;Residues: 1-17 <AATS>
A;Residues: EMBL:XO7448; NID:g33104; PIDN:CAB56703.1; PID:g6002173
A;Note: the authors translated the codon AGT for residue 89 as Met
R;Mariette, X.; Tsapis, A.; Brouet, J.C.
B;M. J: Immunol. 23, 846-851, 1993
A;Title: Nuclectidic sequence analysis of the variable domains of four human monoclonal
A;Reference number: S4001; MUID:93209281; PMID:7681398
submitted to the EMBL Data Library, June 1992
A; Description: Mechanisms that generate human immunoglobulin diversity operate from the A; Description: Mechanisms that generate human immunoglobulin diversity operate from the A; Reference number: S31505
A; Reference number: S31500
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-136 < CUI>
A; Residues: 1-136 < CUI>
A; Cross-references: EMBL: Z14165; NID: 930994; PIDN: CAA78534.1; PID: 930995
C; Superfamily: immunoglobulin v region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin homology < IMM>
F; 34-117/Domain: immunoglobulin homology < IMM>
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A,Introns: 16/1
C,Superfamily: immunoglobulin V region; immunoglobulin homology
C,Keywords: heterotetramer; immunoglobulin
F;1-13/Domain: signal sequence #sterus predicted <81G>
F;2-117/Product: Ig heavy chain V region (V35) #status predicted
F;34-117/Domain: immunoglobulin homology <1MM>
                                                                                                                                                                                                                                                                                                                                                       Length 136;
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Pred. No. 5.4e-41;
4; Mismatches 8;
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-------WGQGTMVTVSS 135
                                                                                                                                                                                                                                                                                                                                                                                                                 14;
                                                                                                                                                                                                                                                                                                                                                   65.7%; Score 549.5; DB 2
69.9%; Pred. No. 4.7e-41;
ive 12; Mismatches 14
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A,Gene: GDB:IGHV@
A,Cross-references: GDB:128528; OMIM:147070
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larity 82.7%;
Conservative
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Best Local Similarity 69.9%
Matches 109; Conservative
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A;Molecule type: mRNA
A;Residues: 20-116 <MAR>
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 13-dan-1995 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999
C;Accession: 818551; 823625
R;Shin, E.K.; Matsuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; H. Rambo J. 10, 3641-3645, 1991
A;Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: cl
A;Reference number: 818551; MUID:92037524; PMID:1935893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-17 < SHI>
A; Residues: 1-17 < SHI>
A; Residues: 1-17 < SHI>
A; Crasherees: EMBL: K62106; NID: g37831; PIDN: CAA44016.1; PID: g37832
A; Croses T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, D.A.; U. Exp. Med. 175, 831-842, 1992
A; Tile: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from the A; Reference number: S23623; MUID: 92156804; PMID: 1740665
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C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31600
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
                                                                                                                                                                                                                                  1 MDWIWRILFLVAAAIGAHSQVQLVQSGAEVKKPGASVKVSCKGSGYT-----FTA
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A; Residues: 1-117 < OLE>
A; Residues: 1-117 < OLE>
A; Residues: 1-117 < OLE>
A; A; A; Cross-references: EMBL:X59704; NID:g32552; PIDN:CAA42225.1; PID:g32553
C; Genetics: 16/1
C; Genetics: 16/1
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Reywords: heterotetramer; immunoglobulin
C; Reywords: heterotetramer; immunoglobulin
F; 1-19/Domain: signal sequence #status predicted <SIG>
F; 20-117/Product: Ig heavy Citain V region (VI-2) #status predicted <MAT>
F; 34-117/Domain: immunoglobulin homology <IMM>
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                                                                                                                                11;
                                                                            Length 171;
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83.5%; Pred. No. 3.6e-41;
iive 4; Mismatches 7; Indels
                                                                                                                                Indels
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                                                                                                                                   19;
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                                                                      Score 591.5; DB 2
Pred. No. 1.3e-44;
9; Mismatches 19
                                                                                                                                                                                                                                                                                                                                                                                                                          121 AMYYCARADNYFDIVTGYTSHYFDYWGRGTLVTVSS
                  F;34-117/Domain: immunoglobulin homology <IMM>
                                                                            70.7%;
                                                                Query Match
Best Local Similarity 75.09
Matches 117; Conservative
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106; Conservative
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A.M.C.GCUILE type: MRNA
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A.N.C.GCUILE type: MRNA
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19 heavy chain V region precursor - human (fragment)

()Species: Homo sapiens (man)

()Species: Homo sapiens (man)

()Species: 22-Nov-1993 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000

()Accession: $29257

Ext. J. Biochem. 207, 1115-1121, 1992

A;Title: Molecular characterization of a human anti-Rh(D) antibody with a D(H) segment

A;Reference number: $29257, MUID:92362614; PMID:1499555

A;Accession: $29257
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C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 26-Apr-1996
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A,Residues: 1-148 <CHO>
A,CTOSE-references: GB1-824401; NID:9251699; PIDN:AAB22940.1; PID:9253700
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;34-117/Domain: immunoglobulin homology <IMM>
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J. Exp. Med. 169, 1631-1643, 1989
A,Title: Relationship of variable region genes expressed
A;Reference number: PLO106; MUID:89235583; PMID:2541221
A;Recession: PL0105
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61.8%; Score 517; DB 2; L
Best Local Similarity 65.4%; Pred. No. 3.5e-38;
Matches 104; Conservative 15; Mismatches 26;
                                                                                                                           121 AMYYCARADNYFDIVTGYTSHYFDYWGRGTLVTVSS 156
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Pred. No. 1.7e-38;
8; Mismatches 30;
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Best Local Similarity 67.9%;
Matches 106; Conservative
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Cipate: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
Cidecesion: S1680
R; Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C. submitted to the EMBL Data Library, June 1992
A; Description: Mechanisms that generate human immunoglobulin diversity operate from A; Reference number: S1585
A; Reference number: S1585
A; Reference number: S1585
A; Crossidues: Dealiminary
A; Molecule type: mRNA
A; Status: preliminary
A; Cross-references: EMBL: Z14213; NID: G37795; PIDN: ChA78582.1; PID: G37796
C; Genetics:
A; Introns: 16/1
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 34-117/ Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ); DB 2; Lens. 2.7e-40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 117;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 81.1%; Pred. No. 2.7e-
Matches 103; Conservative 7; Mismatches
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Best Local Similarity 67.3%
Matches 105; Conservative
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| AVYYCAR 117
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                                                                                                      121 AMYYCAR 127
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Cyspecies: Homo sapiens (man)
Cyspecies: Homo sapiens (man)
Cyaccession: A32483 #sequence_revision 12-Oct-1989 #text_change 16-Aug-1996
Cyaccession: A32483
Rylatzrick, J.W.; Danielsson, L.; Brenner, C.A.; Abrahamson, M.; Fry, K.E.; Borrebaeck, Biochem. Biophys. Res. Commun. 160, 1250-1256, 1989
A;Title: Rapid Cloning of rearranged immunoglobulin genes from human hybridoma cells us A;Reference number: A32483; MUID:89273586; PMID:2499327
A;Accession: A32483
A;Acturus: preliminary
A;Acturus: preliminary
A;Molecule type: mRNA
A;Residues: 1-142 < LAR>
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C.Superfamily: immunoglobulin V region; immunoglobulin homology
C.Steywords: heterotetramer; immunoglobulin
F.15-98/Domain: immunoglobulin homology <INM'>
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R;Kipps, T.J.; Tomhave, E.; Fratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.
Proc. Natl.;Acad. Sci. U.S.A. 86, 5913-5917, 1989
A;Title: Developmentally restricted immunoglobulin heavy chain variable region A;Accession: D33548; MUID:89345575; PMID:2203826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       139
                                                                                                                                               51 INPNSGGTNYAQKFQGWVTMTRDTSISTAYMELSRLRSDDTAVYYCARDSAYYDSSGYY 110
                                                                                         INPNSGATDYAHKEÇGRVTMSRDTSISTAYMELSRLTSDDTAMYYCARADNYFDIVTGYT 139
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C;Species: Homo sapiens (man)
C;Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
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ilarity 72.5%; Pred. No. 5.9e-37;
Conservative 10; Mismatches 12:
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         1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTG-
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                                                                                                                                                                                                                                                                                140 S--HYFDYWGRGTLVTVSS 156
                                                                                                                                                                                                                                                                                                                                            111 SANYYMDVWGKGTTVTVSS 129
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106 CYYFFDYWGQGTLVTVSS 123
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Best Local Similarity 67.8%
Matches 103; Conservative
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Best Local Similarity
Matches 100; Conserv
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C; Decies: n: 846393
R; Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
Nol. Biol. 239, 68-79, 1994
A; Fitle: In vitro assembly of repertoires of antibody chains on the surface of phage by A; Fitle: In vitro assembly of repertoires of antibody chains on the surface of phage by A; Fitle: proliminary
A; Accession: 846393
A; Station of the surface of phage by A; Station of the surface of phage by A; Station of the surface of phage by A; Station of the surface of phage by A; Station of the surface of phage by A; Station of the surface of phage by A; Station of the surface of phage by A; Station of the surface of phage by A; Station of the surface of phage by A; Station of the surface of phage by A; Station of the surface of phage by A; Station of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface 
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                                                           -----FAM 50
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                                                                                                                                                                                                           1 MDWTWRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA
                                                                                                                                                    YSVHWVRQAPGOGLEWMGRINPNSGATDYAHKFQGRVTMSRDTSISTAYMELSRLTSDDT
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Pred. No. 3.4e-37;
8; Mismatches 18; Indels
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         1 MDWIWRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKASGYT-
                                                                                                                                                                                                                                                                                                                                            121 AMYYCARADNYFDIVTGY---TSHYFDYWGRGTLVTVSS 156
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|11 AVYYCARSPR-INMVRGVLITTPPWFDSWGQGTLVIVSS
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Best Local Similarity 72.7%;
Matches 101; Conservative
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Length 134; Indels

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1 MDWTWRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA 60
C;Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: sigal sequence #status predicted <81G>
F:20-134/Product: Ig heavy chain V region (fragment) #status predicted <WAT>
F:34-117/Domain: immunoglobulin homology <1MM>
                                                                                                                                                                                                                                                                                                       1 MDWTWRILFLVAAATGAHSQVQLIQSGSELRKPGASVKVSCKASGYTFTN-------
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                                                                                                                                             Query Match
58.7%; Score 491; DB 2; Lk
Best Local Similarity 59.6%; Pred. No. 5.9e-36;
Matches 93; Conservative 19; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 AMYYCARADNYFDIVTGYTSHYFDYWGRGTLVTVSS 156
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N.Alternate names: rheumatoid factor
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Accession: 23.Apr-1993 #sequence_revision 23.Apr-1993 #text_change 21-Jan-2000
C.Accession: 521916
R.Mierau, R.; Gause, A.; Kueppers, R.; Michels, M.; Mageed, R.A.; Jefferis, R.; Genth, E submitted to the EMBL Data Library, July 1991
A.Pefeription: A Human monoclonal IgA rheumatoid factor using the Vk(IV) light chain gen
                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Shin, Ext.; Matsuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; H
EMBO J. 10, 3641-3645, 1991
A;Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: cl
A;Reference number: S18551; MUID:92037524; PMID:1935893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Residues: 1-117 <-SHI>
A, Residues: 1-117 <-SHI>
A, Cross-references: EMBL:X62109
A, Cross-references: EMBL:X62109
B; Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A, Thitle: The repertoire of human germline V(H) sequences reveals about fifty groups of A, Reference number: $26885, MUID:93021117; PMID:1404388
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               PGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTSISTAYMELSRLTSDDTAMYYCAR-- 127
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                                                                                                                                                                                                                                                                                                                                                                        Species: Homo sapiens (man)
Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999
Accession: S18553; S26916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 20-117 <TOM>
A; Cross-references: EMBL:212327; NID:g32871; PIDN:CAA78197.1; PID:g32872
C; Genetics: 16/1
A; Introns: 16/1
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
C; Keywords: heterotetramer; immunoglobulin
F; 1-19/Domain: signal sequence #Status predicted <SIG>
F; 20-117/Product: Ig heavy chain V region (VI-3b) #status predicted <MAT>
F; 34-117/Domain: immunoglobulin homology <IMM>
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
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Best Local Similarity 74.8%; Pred. No. 3.4e-36;
Matches 95; Conservative 9; Mismatches 13
                                                                                                                                   128 -ADNYFD--IVTGYTSHYFDYWGRGTLVTVSS 156
                                                                                                                                                                      Accession: S18553
Status: translation not shown
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| AVYYCAR 117
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

April 5, 2004, 12:10:21; Search time 7.1269 Seconds (without alignments) 1139.758 Million cell updates/sec

US-10-044-569B-6 837 1 MDWTWRILFLVAAATGAHSQ.......GYTSHYFDYWGRGTLVTVSS 156 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

141681

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	83 homo	omount S1 mus	SO mus	P01746 mus musculu P01759 mus musculu	53 mus 1		mus	BULS	mus.	. SUM	mus :	80m	mus,	mus,	mus.	ม เมนร แ	P06326 homo sapien	homo	เสนายา	mus n	homo.	homo.	160 homo	783 mus n	305 rattue	61 homo s	308 mus mu	PO1807 mus musculu
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HV40_MOUSE HV3I_HUMAN	HVO3_CARAU HV3H_HUMAN HV3U_HUMAN	HV3G_HUMAN HV43_MOUSE	HV01_CAICR HV3D_HUMAN	HV41_MOUSE HV39_MOUSE	HV42_MOUSE
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37.3	37.2 37.0 36.6	36.3	35.8	35.6	35.1
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ALIGNMENTS

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111 AVFYCAKSDPFWSDYYNFDYSYT---LDVWGQGTTVTVSS 147
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SEQUENCE
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SMART; SI
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ID HV07 MC
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                                            YYMHWVRQAPGQGLEWMGRINPNSGGTNYAQKFQGRVTSTRDTSISTAYMELSRLRSDDT 110
      61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTSISTAYMELSRLTSDDT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MDWTWRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA 60
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16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
19 heavy chain V-I region ND precursor (Fragments).
Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Marcel Dekker, New York (1978).
-!- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA
PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27; Indels 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWART; SW00406; IGV; 1.-
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal; Pyrrolidone carboxylic acid.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16491 MW; 948F9F72A5366C20 CRC64;
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IH -> HI (IN REF. 2).

VG -> GV (IN REF. 2).

MISSING (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                147 AA
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GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:006555; P:immune response; NAS.
InterPro; IPR007110; Ig-1ike.
InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                 111 WYYCAR 117
                                                                                                                           AMYYCAR 127
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Best Local Similarity
Matches 97; Conserv
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P01744;
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(WH) gene subgroups...;
Proc. Nacl. Acad. Sci. U.S.A. 80:855-659(1983).

1. SIMILARITY: Contains 1 immunoglobulin-like domain.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-83144028; PubWed=6298778; Rechavi G., Ram D., Glazer L., Zakut R., Givol D.; Rechavi G., Ram D., Glazer L., Zakut R., Givol D.; "Evolutionary aspects of immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Merazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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117 AA; 12946 MW; 2D3F92FC60CD1FE7 CRC64;
                                                                                                      21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-bary chain V-I region HG3 precursor.
Homo sapiens (Human).
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PRT; 139 AA P01751; P01751; P01752; P01751; P01752; P01751; P01752; P01751; P01752; P01751; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; P01752; 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P01752; P01752; P0175
117 AA
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GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0005955; F:ammune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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SMART, SM0406, iGv., 1.
PROSITE, PS06085; iG LIKE, 1.
Immunoglobulin V region; Signal.
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      STANDARD;
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YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTSISTAYMELSRLTSDDT 120
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"Heavy chain variable region contribution to the NPb family of
antibodies: somatic mutation evident in a gamma 2a variable region.";
Cell 24:625-637(1981).
-I- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MDWTWRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA
                                                                                                                                                         MEDLINE=84248078; PubMed=6429663;
Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
                                                                                                                                                                                                            "Illagitimate recombination generates a class switch from C mu to delta in an IgD-secreting plasmacytoma.";
PINC. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
PINS, A2033; HYMST7.
HSSP, P01810; 2FBJ.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-V.
Pfam; PF00047; ig; 1.
SMART; SM00406; iGV.
Immunoglobulin V region; Signal.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky
                                                                                                                                                                                                                                                                                                                                                                                                                                                        IG HEAVY CHAIN V REGION TEPC 1017.
EARMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54.5%; Score 456; DB 1; Length 138; 55.8%; Pred. No. 1.1e-37; ive 23; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPLEMENTARITY - DETERMINING - 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15576 MW; 748157E4C6907B8E CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Igheavy chain V region S43 precursor.
Insumeculus (Mouse).
15-JUL-1999 (Rel. 38, Last annotation update) Ig heavy chain V region TEPC 1017 precursor. Mus musculus (Mouse).
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les 87; Conserv
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                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                   Cucker P.W.;
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HV11 MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981).
-!- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                MEDLINE-81234548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HEAVY CHAIN V REGION B1-8/186-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55.5%; Score 464.5; DB 1; Length 139; 57.7%; Pred. No. 1.7e-38; ive 20; Mismatches 29; Indels 17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
COMPLEMENTARITY-DETERMINING-2.
D SEGMENT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, J00529; AAA38170.1; -.
PIR, A90809; MRNS18.
PDB; 1A6U; 27-MAY-98

DBB; 1A6W; 15-UUL-98.
InterPro; IPR007110; Ig-1ike.
InterPro; IPR003110; Ig-v.
Pfam; PF00047; ig; 1.
PR081TF; PS08185; IGv; 1.
PR081TF; PS08185; IG LIKE; 1.
Immunoglobulin V region; Signal; 3D-structure.
  (Rel. 42, Last annotation update) ain V region B1-8/186-2 precursor.
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(Rel. 02, Last sequence update)
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                       Ig heavy chain V reg:
Mus musculus (Mouse)
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Best Local Similarity
Matches 90; Conserv
                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                    NCBI_TaxID=10090;
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P03980;
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23-OCT-1986
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HV15 MOUSE
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                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch.
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MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL) ACETYL
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Sime J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                             IG HEAVY CHAIN V REGION S43.
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
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-! SIMILARITY: Contains limmunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15200 MW; ADD5881BF44B8EC9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 55.1%; Pred. No. 4.6e-36; tes 86; Conservative 18; Mismatches 33;
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21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Mus musculus (Mouse).
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D SEGMENT.
JH2 SEGMENT.
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PIR; AQ2038; G2M843.
HSSP; PO1810; ZFBJ.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
Pfam; PR00407; Ig; 1.
PROSITE; SMO406; IG'.
PROSITE; PS50835; IG_LIKE; 1.
IMMLOGIObulin V region; Signal.
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137 AA;
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Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCSI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IG HEAVY CHAIN V REGION 93G7 IG-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15514 MW; 25A4CBBE31DA5CE8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 AMYYCARADNYFDIVTGYTSHYFDYWGRGTLVTVSS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49.7%; Score 416; DB 1; 50.6%; Pred. No. 9.3e-34; iive 29; Mismatches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
1g heavy chain V region BCL1 precursor.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam, PF00047; ig; 1. --
SMART, SMORG6; IG; 1. --
PROSTTE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Hybridoma; Signal.
                                                                                                                                                                                                                                                         EMBL; J00493; AAA38128.1; -. PIR; A94264; HVMSG7. HSSP: P01810; 2FBU. InterPro; IPR007110; IG-like. InterPro; IPR003596; IG_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; J00494; AAA38130.1; -. PIR; A02042; HVMSB1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 50.6%
nes 79, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               140
139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140 AA;
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SEQUENCE FROM N.A.
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Best Local Similarity 59.8%; Pred. No. 1.8e-32; Matches 76; Conservative 18; Mismatches 23;
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59.8%; Pred. No. 4.3e-32;
iive 17; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1g heavy chain V region 23 precursor.
                                                                                                                                                                                                                                                                                                                                                117 AA.
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SWART; SM00406; IGV; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
SIGNAL
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                                                                                                                                                                                                                                                                                                                                                STANDARD;
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                                                                                                                                                                                                                121 AMYYCAR 127
                                                                                                                                                                                                                                         111 AVYYCAR 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117 AA;
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les 76; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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P01748;
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                                                                                                                                                                                                                                                                                                                            1 MDWTWRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA 60
                                                                                                                                                                                                                                                                                                                                                  "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; cell 24:622-637(1981).
-1- MISCELLANEOUS: THIS GERMINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES. PIR; D90809; HYMS61.
HISSP, P01810; 2FBJ.
HISSP, P01810; 2FBJ.
InterPro; IPR003196; Ig_v.
Ffam, PFR0047; ig_l.
FMANT; SM00406; IGv; 1.
FROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-81234548; PubMed=6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
Baltimore D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazca; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                         20;
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FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
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                                                                                                                                                                                                                                                     Length 136,
                                                                                                                                                        IG HEAVY CHAIN V REGION BCL1. IG-LIKE.
                                                                                                                                                                                                                                                                                     21; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12890 MW; 16191A088CB17F5A CRC64;
                                                                                                                                                                                                                15078 MW; 6827CFBC6DB3F35E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AMYYCARADNYFDIVTGYTSHYFDYWGRGTLVTVSS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111 ANLYCAR-----YXGNYFDYWGQGTTLTVSS 136
                                                                                                                                                                                                                                                   Query Match

49.3%; Score 413; DB 1;
Best Local Similarity 52.6%; Pred. No. 1.8e-33;
Matches 82; Conservative 21; Mismatches 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 402; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HV09_MOUSE STANDARD; PRT; 117 AA. P01753; P11271; Created) 01-JUL-1986 (Rel. 01, Created) 01-JUL-1989 (Rel. 11, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) Mas musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY
HSSP; PO1772; 2FB4.
InterPro; IPRO07110; Ig-1lke.
InterPro; IPRO03596; Ig_v.
Ffam; PPO0047; 1g; 1.
SWART; SWO0406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Signal.
SIGNAL
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136
136 AA;
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55
69
86
41
117 AA;
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                                                                                    1 MGWSCIILFLVAAANGVHSQVQLQQPGTELVKPGASVKLSCKASGYT-----FTS 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; cell 24:625-631(1891).

Cell 24:625-631(1891).

PILY, MISCELLANBOUS: THIS GENALINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.

PIRY, A02030, HYMS23.

INTERPRO, IPRO07110; 19-1ike.

InterPro, IPR003190; 19-v.
                                                     1 MDWTWRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA
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10; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=CS7BL/6;
MEDIINE=81234548; PubMed=6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metacoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
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FRAMEWORK-1.
COMPLENGUTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMGINTARITY-DETERMINING-2.
FRAMEWORK-3.
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Indels
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[1]
SECUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-81234548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JAN'1988 (Rel. 06, Created)
01-JAN'1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 heavy chain V region VHSSB B4 precursor.
Mus musculus (Mouse).
Musmulia; Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Musli_TaxID=10090;
                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IG HEAVY CHAIN V REGION 102.
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12867 MW; 740A65DD851FCA8C CRC64;
                                                                                                                                     21-JUJ-1986 (Rel. 01, Created)
21-JUJ-1986 (Rel. 01, Last sequence update)
15-JUJ-1999 (Rel. 38, Last annotation update)
16-JUJ-1999 (Anel. 38, Last annotation update)
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 AA.
                                                                                             117 AA
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InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS0835; IG LIKE; 1.
Immunoglobulin V region; Signal.
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                                                                                        STANDARD;
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117
117 AA;
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les 76; Conserv
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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P06328;
                                                                                             MOUSE
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SEQUENCE
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTSISTAYMELSRLTSDDT 120
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MEDLINE=81234548; PubMed=6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IG HEAVY CHAIN V REGION VH558 B4. FRAMEWORK-1. COMPLEMENTARITY-DETERMINING-1.
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MEDLINE-85099340; PubMed=2578321;
Yancopoulos G.D., Alt F.W.;
"Developmentally controlled and tissue-specific expression of unrearranged VH gene segments.";
Cell 40:271-281(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45.5%; Score 381; DB 1; Length 117; 56.7%; Pred. No. 2e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPLEMENTARITY-DETERMINING-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12834 MW; B8862FAC67ABD345 CRC64;
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(Rel. 11, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUL-1989 (Rel. 11, Last sequence up 28-REB-2003 (Rel. 41, Last annotation III heavy chain V region 145 precursor IGH-VU558.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMARY, SM00406; IGv. 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, M13788; AAA38506.1; -. PIR; A02035; MHMSB4.
HSSP, PO1810; ZFBJ.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_V.
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nes 72; Conservative
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Conservative
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es 73; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HV50 MOUSE
P06329;
                                                                                                                                                                                NON TER
SEQUENCE
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HV50_MOUSE
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Matches
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                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBD outstainstthe European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 YMMHWYXQRPGRGLEWIGRIDPNSGGTKYNEKFKSKATLTVDKPSSTAYWQLSSLTSEDS 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MGWSCIMLFLAATATGVHFQVQLQQPGAELVKPGASVKLSSKASGYT------FTS 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            idictype response of the strain A mouse.";

Eur. J. Immunol. 12:1023-1032(1982).

-!- MISCELLANDOUS: FROM ANALYSIES OF THE SIZES OF SEVERAL OTHER

DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS

CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981).
-!- MISCELLANDUS: THIS GERMINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'The genetic basis of antibody production: the dominant anti-arsonate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gapa
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10-1071-1986 (Rel. 01, Last sequence update)
10-1071-2003 (Rel. 42, Last annotation update)
1g heavy chain V region 36-65.
1g heavy chain V region 36-65.
Bukaryota, Metazoa; Chordat, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                      IG HEAVY CHAIN V REGION 145.
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45.4%; Score 380; DB 1; Length 117; 57.5%; Pred. No. 2.5e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26; Indels
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Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,
Marshak-Rothstein A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18; Mismatches
                                                                                                                                                                                                                                                                                                                                           Pfam; PF00047; ig; 1. SMARY; SMO0406; IGv; 1. PROSITE; PS50815; IG LIKE; 1. Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                  EMBL, JO0533, AAA38602.1; -. PIR; C90809; HVM845. HSSP, P01810; 2FBJ. MGD; MGL:96486; IGh-VJ558. InterPro; IPR007110; IG-like. InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 57.5
les 73; Conservative
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 QVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTAYSVHWVRQAPGQGLEWMGR
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Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
"A V region determinant (idiotope) expressed at high frequency in B
"Jymbhocytes is encoded by a large set of antibody structural genes.";
EMBO J. 3:517-523(1984).
                                                                                                                                                                                                                                                                                                                              Query Match
45.4%; Score 380; DB 1; Length 120;
Best Local Similarity 53.7%; Pred. No. 2.6e-30;
Matches 73; Conservative 23; Mismatches 24; Indels 16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1998 (Rel. 38, Last annotation update)
16-JUL-1999 (Rel. 38, Last annotation update)
1g heavy chain V region AC38 15.3.
Mus musculus (Mouse).
Elexaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
1731_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44.6%; Score 373.5; DB 1; Length 120; 53.3%; Pred. No. 1.1e-29; Indels 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13311 MW; 914453F426F09834 CRC64;
                                                                                                                                                                                                                                                                            120 AA; 13307 MW; FF04E4A167B654AF CRC64;
  Contains 1 immunoglobulin-like domain.
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J SEGMENT.
BY SIMILARITY.
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-!- SIMILARITY: Contains 1 immunoglot HSSP; P01789; 1MCP.
InterPro; 1PR00710; Ig-like.
InterPro; 1PR003596; Ig-v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Hybridoma.
DOMAIN
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SMART; SM00406; IG; 1.
PROSTIE; PS50835; IG LIKE; 1.
Immunoglobulin V region.
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InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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СD

рp ò Search completed: April 5, 2004, 13:24:55 Job time: 7.1269 secs

Q8K172 mus musculu G8VGC9 mus musculu G8VGC mus musculu Q7FmX1 mus musculu Q991a6 mus musculu Q991a7 mus musculu Q91wt1 mus musculu Q924r3 mus musculu Q92583 mus musculu Q92583 mus musculu Q92547 mus musculu Q92477 mus musculu Q92477 mus musculu Q92477 mus musculu Q92477 mus musculu Q92477 mus musculu Q92477 mus musculu Q92477 mus musculu Q92477 mus musculu Q92477 mus musculu Q92477 mus musculu

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61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTSISTAYMELSRLTSDDT 120
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Best Local Similarity 64.1%; Pred. No. 4.9e-42;
Matches 100; Conservative 18; Mismatches 26; Indels 12; Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Q99KLI
Q99LWKI
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                                                                                                                                                                                                                                                                                                                                         1 MDWTWRILFLVAAATGAHSQ.......GYTSHYFDYWGRGTLVTVSS 156
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Q95ga6 homo s
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Q7z7p5 homo s
Q9x298 homo s
Q9u194 homo s
Q9u195 homo s
Q91195 homo s
Q95gR homo s
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                      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                            OM protein - protein search, using sw model
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sp_vertebrate:*
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No.
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A MEDLINE=22388257; PubMed=12477932;

A Karausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Altachul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altachul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altachul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altachul S.F., Jeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

A Botheron M., Soares M.B., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rachy J., Helton E., Ketteman M., Rodrigues S., Sanchez A.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Generation and initial analysis of more than 15,000 full-length human
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                  Length 500;
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Strausberg R.;
Stwaitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BOO51328; AAH51328.1; -.
Hypothetical protein.
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO05951; AAH05951.1; -.
HSSP; P01789; 1MCP.
                                                                                                                               Edm. PF00-1170-157. 4.

SWART; SM00406; IGV; 1.

PROSITE; PS50835; IG LIKE; 4.

PROSITE; P500290; IG MHC; 1.

RYPOCHELICAL Drotein.

SEQUENCE 500 AA; 54154 MW; 0A9BF43F2A3CC6D9 CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       roc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 AMYYCARA-DNYFDIVTGYTSHYFDYWGRGTLVTVSS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    111 AVYYCARRYCSYSSCONDYYXXYMDVWGKGTTVTVSS 147
                                                                                                                                                                                                                                                                60.2%; Score 503.5; DB 4; 65.0%; Pred. No. 1.7e-41; Micmatches 33;
                                                                    InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-2003 (TrEMBLrel. 25, 01-0CT-2003 (TrEMBLrel. 25, 01-0CT-2003 (TrEMBLrel. 25, Hypothetical protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                      Best Local Similarity 65.0%
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and mouse cDNA sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MDWTWRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:000562; C:intracellular; IEA.
GO; GO:000562; C:intracellular; IEA.
GO; GO:0005825; C:intracellular; IEA.
GO; GO:0005825; C:intracellular; IEA.
InterPro; IPRO0710; Ig-like.
InterPro; IPRO07006; Ig-MtC.
InterPro; IPRO03006; Ig-W.
Pfam; PRO0406; IG-V.
Pfam; PRO0406; IGV; 1.
PROSITE; PS:00047; HTH ARAC_FAMILY_1; 1.
PROSITE; PS:00035; IG_MHC; 3.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60.7%; Score 508; DB 4; Length 614; 65.0%; Pred. No. 8.1e-42; ive 15; Mismatches 17; Indels ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.; Strausberg R.; Submitted (dut-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC000851; AAH09851.1; -...PIR; S15590; S15590.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.
SEQUENCE 614 AA; 67921 MW; S5EF536E77AA9BBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 TAMYYCARADNYFDIVTGYTSHY---FDYWGRGTLVTVSS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-UUN-2001 (TrEMBLrel. 17, Created)
01-UUN-2001 (TrEMBLrel. 17, Last sequence update)
01-UCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
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                                                        AMYYCARADNYFDIVTGYTSHYFDYWGRGTLVTVSS
                                                                                                                                                                              PRT;
                                                                                                                                                                                                                         Created)
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Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
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Q9BRV0;
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61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTSISTAYMELSRLTSDDT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Homo saplens putative microfibrillar protein with Ig-like domain 3 mRNA (Matrix Cell Adhesion Molecule-3, Mat-CAM 3).";

Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AN39025; AAK82649.1; -.

InterPro; PR007110; Ig-like.

InterPro; IPR001596; Ig-v.

Pfam; PR00047; ig; 1.

SNART; SNO046; Ig-v.

PROSITE; PS50835; IG LIKE: 1.

SEQUENCE IS9 AA; I7497 MW; 5D29537E881FAF02 CRC64;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MDWTWRVFCLLAVGPGAHSQVQLVQSGAEVKKPGASVKVSCKASGYTFSN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 159;
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1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
(Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 AMYYCARADNYF---DIVTGYTSHYFDYWGRGTLVTVSS 156
                                                                Q96QSO;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative matrix cell adhesion molecule-3.
Homo sapiens (Human).
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Clin. Immunol. Immunopathol. 87:184-192(1998).
EMEJ. AP035020; AAD56256.1; -.
HSSP; PO1810; 2FBJ.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
Ffan, PP00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG-LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58.5%; Score 489.5; DB 60.4%; Pred. No. 9.5e-41 ive 17; Mismatches 3
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                                  159 AA.
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                                  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 60.49
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                                  PRELIMINARY;
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NON TER
SEQUENCE
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Q9UL94;
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Q9UL94
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A Jacquemin M.G., Vander Elst L.P.L.;
Tacquemin M.G., Vander Elst L.P.L.;
Tacquemin M.G., Vander Elst L.P.L.;
Time and kinetics of factor VIII inactivation: study with an igd4 monclonal antibody derived from a hemophilia A patient with inhibitor.";
Elood 92:496-506(1998)
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Bukaryota, Merezoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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                                                                    Length 469;
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                                                                                                                                        Indels
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51395 MW; C8D5BE12BAAF795C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09Y298;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 AMYYCARADNYFDIVTGYTSHYFDYWGRGTLVTVSS 156
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                                                                    59.0%; Score 493.5; DB 4;
larity 64.1%; Pred. No. 1.6e-40;
Conservative 13; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 AMYYCARADNYFDIVTGYTSHYFDYWGRGTLVTVSS 156
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nes 99; Conservative
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150 AA;
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                                                                                                  Local Similarity
les 100; Conserv
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   469
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   SEQUENCE
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Matches

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Q9Y298

13205 MW; 13E64F5345F4A16E CRC64;

9 20

Indels

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                                                                                                                                                                                                                                                                                                                                 51 INPNSWITINYAQKFQGKVIMTKDISISIAYMELSRLRSBDTAVYYCARG------GGR 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80 INPNSGATDYAHKFQGRVTMSRDTSISTAYMELSRLTSDDTAMYYCARADNYFDIVTGYT 139
                                                                                                                                                                                                                                                                                                 80 INPNSGATDYAHKFQGRVTMSRDTSISTAYMELSRLTSDDTAMYYCARADNYFDIVTGYT 139
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                                                                                                                                                                                                         Gaps
                                                                                                      Gaps
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Mammalia; Eutheria, Primates; Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Myosin-reactive autoantibodies in rheumatic carditis and normal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                   Length 119,
                                                                                               14; Indels
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125 AA; 13516 MW; 0D3CD5C232488EAC CRC64;
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Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Letus.; Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035019; AAD56255.1; -.
HSSP; POIBIO, 27EBJ.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
Ffam; PF00047; Igy; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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SEQUENCE 125 AA; 13516 MW; OD3CD5C232488EAC
                               56.9%; Score 476; DB 4; 69.3%; Pred. No. 1.4e-39; ive 10; Mismatches 14
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BIGDLINE=98277139; PubMed=9614934; Wu X., Liu B., Van der Merwe P.L., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                140 SHYFDYWGRGTLVTVSS 156
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095978;
0HAX-1999 (TEMBLEEL 10,
01-MAX-1999 (TEMBLEEL 10,
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   Ouery Match
Best Local Similarity 69.3%
Pest Local Similarity 69.3%
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Best Local Similarity
Matches 95; Conserv
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Q9UL95;
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095978
ID 0959
AC 0959
DT 01-M
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61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTSISTAYMELSRLTSDDT 120
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                                                                                                                                                                                                                              SEQUENCE FROM N.A.

TISSUE=Peripheral blood;

TISSUE=Peripheral blood;

TISSUE=Peripheral blood;

A ., Zander T., Kueppers R., Irsch J., Kanzler H., Kornacker M.,

Jox A., Zander T., Wolf J.;

Bohlen H., Diehl V., Wolf J.;

Absence of immunoglobulin in Hodgkin's disease is associated with

patient with mixed cellularity Hodgkin's disease is associated with

somatic mutations within the untranslated regions of rearranged and

class switch recombinated ig genes.";

Submitted (ARR-1998) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ005570; CAA06599.1; -.

RICEPPO; IPR007110; Ig-like.

RICEPPO; IPR007110; Ig-like.

RICEPPO; IPR00471; Ig-like.

RICEPPO; IPR00471; Ig-like.

RICEPPO; IPR00471; Ig-like.

RICEPPO; IPR00471; Ig-like.

REMEL; SM004406; IGy, 1.
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Ishibashi T., Kanehori, K., Yosida M., Watanabe S., Ishida S., Ono Y., Hotuta T., Hiraoka S., Murakawa K., Takiguchi S., Kusano J., Watanaben T., Hiraoka S., Murakawa K., Takiguchi S., Kusano J., Watanabe M., Fujimori K., Tanai H., Ishida M., Yamashita H., Chiba Y., Suzuki Y., Hata H., Makagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T., Irie R., Otsuki T., Sagano S., Morinaga M., Kawamura M., Rawakami B., Nagai K., Isogai T., Sugano S., Sugiyama T., Sugiyama A., Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AKO58027; BAB71633.1;
EnterPro; IPR003106; Ig-Mic.
InterPro; IPR003006; Ig-Mic.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                  Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16;
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157 AA; 17304 MW; 86986EDDA84D88B5 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein FLJ25298.
. 25, Last annotation update) (Fragment).
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      (TremBLrel.
      01-OCT-2003 (TrEMBLrel
VH1 protein precursor
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SEQUENCE
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SIGNAL
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Q9D8L4
Q9D8L4
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RESULT 12
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                                                                                                                                                                                                                         51 YAFTWVRQAPGQGLQWMGGIIPNPGAPNXAQNFQDRVTISADDSTTTVYMELTSLTFEDT 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80 INPNSGATDYAHKROGRVTMSRDTSISTAYMELSRLTSDDTAMYYCARADNYFDIVTGYT 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 INPSGGSTSYAOKFOGKVTMTRDTSTSTVYMELSSLRSEDTAVYYCARG---LYVVVPAA 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EVQLVESGAEVKKRGASVKVSCKASGYT------FSSYYMHWVRQAPGQGLEWMGI 50
                                                                                                                                                                   1 MDWTWRFLFVVAAVTGVQSQVHLVQSGAELKMPGSSVKVSCK-----ASANWFRS 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 QVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTAYSVHWVRQAPGQGLEWMGR 79
                                                                                                                                                    9
                                                                                                                                                                                                        61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTSISTAYMELSRLTSDDT
                                                                                                                                                    1 MDWTWRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
Mu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13;
                                                                                         / Match 55.7%; Score 466.5; DB 4; Length 496; Local Similarity 59.2%; Pred. No. 8.2e-38; les 93; Conservative 18; Mismatches 31; Indels 15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 124;
                                                                                                                                                                                                                                                                                                                                                                                        01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13580 MW; 1BAAACBD96ACD2A2 CRC64;
                                                     Hypothetical protein..
SEQUENCE 496 AA; 53532 MM; C72E21E247C86FED CRC64;
                                                                                                                                                                                                                                                                 121 AMYYCARADNYFDIVTGYTSHYF-DYWGRGTLVTVSS 156
                                                                                                                                                                                                                                                                                AFYYCGRGLIYY----GSGSYYYLQHWGQGTLVTVSS 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54.9%; Score 459.5; DB 4;
66.4%; Pred. No. 6.6e-38;
ive 12; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035022; AAD56258.1; -.
EMSP; P01772; 2FB4.
InterPro; IPR007110; Ig-like.
InterPro; IPR00396; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                124 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FSRFDYWGQGTLVTVSS 124
        SMART; SMO0406; IGV; 1.
PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00047; ig; 1. SMART; SM00406; IGv; 1. PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 66.4%
nes 91; Conservative
                                                                                                                                                                                                                                                                                                                                                                · PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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NON TER
SEQUENCE
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                                                                                               Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Functional annotation of a full-length mouse cDNA collection:"; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . Match
Local Similarity 54.5%; Pred. No. 5.4e-37;
les 85; Conservative 25; Mismatches 28; Indels 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INCEPTO 1500-03-05 13_.
SWART; SMO0406; IGV: 1.
PROSITE; PSS0335; IG LIKE; 4.
PROSITE; PS00290; IG MHC; 1.
SEQUENCE 473 AA; $1699 NW; 9DED57A514475FBB CRC64;
                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 AMYYCARADNYFDIVTGYTSHYFDYWGRGTLVTVSS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0921K1;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ä
473 AA.
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PIR; S26746; S26746.
HSSP; P01842; 7FRB.
INCEPPO; 196443; 1gh-1.
InterPro; 1PR007110; 1g-11ke.
InterPro; 1PR003006; 1g_MHC.
                                                                          01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-OCT-2003 (TrEMBLrel. 25,
    PRELIMINARY;
                                                                                                                                                                                                          1810060009Rik protein.
IGH-1 OR 1810060009RIK.
Mus musculus (Mouse).
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Q921K1
ID Q921K
AC Q921K
DT 01-DE
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Search completed: April 5, 2004, 13:42:06 Job time : 34.2589 secs
                                                                                            RESULT 15
Q8VCX7
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                                                                                                                                                                                                                                                                                                                                                                                                          61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTSISTAYMELSRLTSDDT 120
                                                                                                                                                                                                                                                                                                                                                      1 MGWNCIILFLVATATGVHSQVQLQQPGAELVKPGASVKLSCKASGYT------FTS 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MDWTWRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA 60
                                                                                                                                                                                                                                                                                                                                1 MDWTWRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similar to RIKEN cDNA 1810060009 gene.

Was musculus (Mouse).

Eukarycia, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13;
                                                                                                                                                                                                                                                                       Match 54.7%; Score 457.5; DB 11; Length 278; Local Similarity 57.7%; Pred. No. 3e-37; Loss 90; Conservative 16; Mismatches 33; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 11; Length 473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.,
Submitted (PEB-2011) to the EMBL/GenBank/DDBJ databases.
Submitted (PEB-2011) to the EMBL/GenBank/DDBJ databases.
EMBL; BC001389 AAH03888.1; --
HSSP; P01842; 7FAB.
InterPro; IPR007110; Ig-like.
InterPro; IPR003056; Ig-v.
Pfam; PF00047; ig; 3.
SNRAT; SM0406; IG-v.
PROSITE; PS00235; IG LIKE; 4.
PROSITE; PS00239; IG LIKE; 4.
PROSITE; PS00230; IG MHC; 1.
SEQUENCE 473 AA; 52449 MW; BE9889B7986DA155 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53.2%; Score 445.5; DB 11; Length 52.6%; Pred. No. 9.5e-36; ive 27; Mismatches 34; Indels
                                                                                                          Strausberg R.;
Strausberg R.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC012207, AAH12207.1;
InterPro; IPR003106; 1g-1ike.
InterPro; IPR003596; 1g-v.
Fram; PF00047; 1g; 2.
SMART; SM00406; 1G; 1.
PROSITE; PS06035; 1G Like; 2.
Hypothetical protein.
SRQUENCE 278 AA; 29778 MW; F894F955DDCD948A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q99L25 PRELIMINARY; PRT; 473 AA.
Q99L25; C1 (TEMBLrel. 17, Created)
01-JUN-2001 (TEMBLrel. 17, Last sequence update)
01-JUN-2001 (TEMBLrel. 25, Last annotation update)
01-OCT-2003 (TEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 AMYYCARADNYFDIVTGYTSHYFDYWGRGTLVTVSS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 Avykcrkgygyddv-----yrdvwgagrryryss 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82; Conservative
             Hypothetical protein. Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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                                                                                               SEQUENCE FROM N.A.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 HTIHWVKQRPEQGLEWIGYIYPRDGSTKYNEKFKGKATLTADKSSSTAYMQLNSLTSEDS 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MDWTWRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA 60
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                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19;
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53.8%; Pred. No. 1.7e-35;
tive 22; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUES-Salivary gland;
Strausberg N.A.
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, BC018315; AAH18315.1; -.
InterPro; IPR007110; Ig-1ike.
InterPro; IPR003106; Ig-MC.
InterPro; IPR003506; Ig-WC.
InterPro; IPR003506; Ig-V.
Pfam, PF00047; ig: 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
SEQUENCE 613 AA; 67855 MW; 41A9384DD4C22862 CRC64;
                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 AMYYCARADNYFDIVTGYTSHYFDYWGRGTLVTVSS 156
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                                                                         121 AMYYCARADNYFDIVTGYTSHYFDYWGRGTLVTVSS
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                                                                                                                                                                                                                                                                 Created)
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PROSITE, PS50835, IG_LIKE, 5.
PROSITE, PS00290; IG_MHC; 3.
                                                                                                                                                                                                                                                           01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                   Hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
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nes 84; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
OM protein - protein search, using sw model
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Run on:	April 5, 2004, 12:09:21; Search time 50.4162 Seconds (without alignments) 874.270 Million cell updates/sec
Title:	US-10-044-569B-6
Perfect score:	837
Sequence:	1 MDWTWRILFLVAAATGAHSQGYTSHYFDYWGRGTLVTVSS 156

Sequence:	1 MDWTWRILFLVAAATGAHSQGYTSHYFDYWGRGTLN
Scoring table: BLOSUM62 Gapop 10	BLOSUM62 Gapop 10.0 , Gapext 0.5
Searched:	1586107 segs, 282547505 residues

1586107		
parameters:		
chosen		
satisfying		
hits		
r of		
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Total		
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Database :							

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

14-JUL-1999; 99US-0143891P.

(LEUV-) LEUVEN RES & DEV VZW. Jacquemin MG, Saint-Remy JR;

WPI; 2001-138333/14. N-PSDB; AAC85452.

Novel cell lines for producing monoclonal antibodies that bind to a factor involved in hemostasis and coagulation cascade, useful for treating and preventing coagulation disorders.

Example 5; Fig 8; 55pp; English.

Aan49760 TNF-selec Aao1759 Antibody- Aam49759 TNF-selec Aaw46650 Reavy cha	Aay96299 Human IGF Abp43131 Human ova Abp45624 Human BLy Aaw62196 Humanised		AAYOLOB HUMBILSEU AAYO2571 HUMBILSEO ADP45718 HUMBI BLY AAW65773 ARTI-humB AAW62205 HUMBILSEO	Aaw62202 Humanised Aay02568 Humanised Aay02572 Humanised
5 AAM49760 5 AAO17494 5 AAM49759 2 AAW48650	3 AAY96299 5 ABP43131 5 ABP45624 2 AAW62196	.,.,.,.	3 AAYBU288 2 AAY02571 5 ABP45718 5 AAW6273 2 AAW62205	2 AAW62202 2 AAY02568 2 AAY02572
			11221 1339 139	
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ALIGNMENTS

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This sequence represents the heavy chain variable region of the monoclonal antibody (MAB), KRIXI. This MAB produced by the cell line of the invention, specifically recognises the wild type factor VIII light chain. KRIXI can be used to inhibit the binding of factor VIII light willebrand factor in a dose dependant manner. The new cell line KRIXI, is deposited with the Belgian Coordinated Collections of Micro-organisms, under accession number LMBP 5089CB. KRIXI, or fragments of it, optionally with a thrombolytic agent, are useful for the treatment and/or prevention of hemostasis, coagulation disorder or thrombocic pathologic condition such as intravascular coagulation, arterial thrombosis, arterial centennesis, and attended of coagulation in a mammal. An effective and safe antithrombotic therapy is provided which reduces the risk of bleeding in mammals, more particularly
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                                                                                                                                                                                                                                                                                                                                                                              YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTSISTAYMELSRLTSDDT 120
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                                                                                                                                                                                                                                                                                                                   MDWTWRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA
                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                        ; Score 837; DB 4; Length 156; Pred. No. 3.7e-71; 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                        121 AMYYCARADNYFDIVTGYTSHYFDYWGRGTLVTVSS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAO18878 standard; protein; 156
                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0%;
Matches 156; Conservative 0
                                                                                                                                                                                                                              Sequence 156 AA;
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WPI; 2003-441521/
N-PSDB; ADE28426.
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                                                                                                                                                                                                                                                                                                                                                                              15-MAY-2003
ADE28427;
                                                                                              Human; antibody; BO2C11; KRIXI; light chain; heavy chain; inflammation; variable region; factor VIII inhibitor; sepsis; septic shock; thrombus formation; systemic inflammatory response syndrome; CDR, disseminated intravascular coaqulation; haemophilia A; immunosuppressive; complementarity determining region; antibacterial; antinflammatory.
                                                   Human KRIX1 heavy chain variable region.
                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                          42. .64
/label= CDR1
79. .95
/label= CDR2
128. .145
/label= CDR3
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jacquemin MG,
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                                                                                                                                                                                                                                                       Homo sapiens
07-NOV-2002
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Key Region Region Region

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New chimeric or human monoclonal antibody or its antigen-binding portion that specifically binds to and activates human CD40, useful for enhancing an immune response in a human, or treating cancer, HIV, neutropenia or viral infections.
                                                                                                                                                   The present invention relates to a pharmaceutical composition for the prevention and/or treatment of systemic Inflammatory response syndrome (SIRS), sepsis, septic shock, thrombus formation in the microvasculature and disseminated intravascular coagulation in mammals, comprising as an estive ingredient a partial inhibitor of factor VIII, in admixture with a carrier. Such inhibitors may include the antibodies B02CII and KRIXI. The present sequence is the heavy chain variable region of KRIXI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTSISTAYMELSRLTSDDT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120
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                                 Pharmaceutical composition for treating systemic inflammatory response syndrome, sepsis, septic, shock and/or thrombus formation in microvasculature in mammals, comprises a partial inhibitor of factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTSISTAYMELSRLTSDDT
                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MDWTWRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA
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                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human anti-CD40 antibody 21-2-1 variable region heavy chain protein.
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                                                                                                                                                                                                                                                                                                                                 Length 156;
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                                                                                                                                                                                                                                                                                                                              100.0%; Score 837; DB 5;
11arity 100.0%; Pred. No. 3.7e-71;
Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ä.
                                                                                                                       Disclosure, Fig 12, 41pp, English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PFIZ ) PFIZER PROD INC. (ABGE-) ABGENIX INC.
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                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 156; Conserv
N-PSDB; AAL49256
                                                                                                                                                                                                                                                                                                  Sequence 156 AA;
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The invention relates to a novel chimeric or human monoclonal antibody or its antigen-binding portion that specifically binds to and activates human CD40. The anti-CD40 antibody of the invention demonstrates cytostatic, virucide, antibacterial, immunostimulant and anti-HIV such as cancer, viral and bacterial infection or genetic, primary or combined immunodeficiency conditions including neutropenia or HIV infection. The anti-CD40 antibodies may also be useful for detecting CD40 in a biological sample in vitro or in vivo, as well as during gene therapy procedures. The current sequence is that of the human anti-CD40 antibody variable region heavy chain protein of the invention.
                        Claim 1; SEQ ID NO 34; 177pp; English.
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 471 AA;
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                                                                                                                                                                      YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTSISTAYMELSRLTSDDT 120
                                                                                             1 MDWTWRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKASGXTFTG------ 50
                                                                        1 MDWTWRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA 60
                                       Indels 11; Gaps
 Length 471;
73.1%; Score 611.5; DB 7; 76.9%; Pred. No. 2.8e-49; ive 7; Mismatches 18;
                                                                                                                                                                                                                        121 AMYYCARADNYFDIVTGYTSHYFDYWGRGTLVTVSS 156
                                                                                                                                                                                                                                                            111 AVYYCAR-DQPLGYCTNGVCSYFDYWGQGTLVTVSS 145
Query Match
Best Local Similarity 76.9°
Matches 120; Conservative
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Anti-human AILIM monoclonal antibody clone Jmab-136, heavy chain.
AAU74296 standard; protein; 470 AA
             (first entry)
             12-MAR-2002
      AAU74296;
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Human; antirheumatic; antiarthritic; antidiabetic; antipsoriatic, antiallergic; antiulcer; neuroprotective; antithyroid; vasotropic; immunosuppressive; dermatological; antiinflammatory; heptotropic; activation inducible lymphocyte immunomodulatory molecule; ALLIM; monoclonal antibody; allergy; rheumatoid arthritis; diabetes mellitus; multiple sclerosis; autoimmune thyroiditis; psoriasis; hepatitis; allergic contact-type dermatitis; chronic inflammatory dermatosis; systemic lupus erythematosus; autoimmune disorder; inflammation; graft versus host reaction; immune clastinal immunity; ulcerative colitis; pneumonia; nephritis; vasculitis; pancreatitis. Homo sapiens.

WO200187981-A2.

22-NOV-2001

15-MAY-2001; 2001WO-JP004035. 18-MAY-2000; 2000JP-00147116. 30-MAR-2001; 2001JP-00099508.

(NISB) JAPAN TOBACCO INC.

Hori N;

Isuji I, Tezuka K,

1. .19 /label=_sig_peptide Location/Qualifiers

Key Peptide Peptide Region Region

WPI; 2002-075313/10. N-PSDB; AAS99472.

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The invention relates to a novel human antibody (I), preferably a human monoclonal antibody which binds to an activation inducible lymphocyte immunomodulatory molecule (AILIM). (I) is useful for modulating signal transduction into a cell mediated by AILIM, for modulating proliferation of AILIM-expressing cells, for modulating production of a cytokine from AILIM-expressing cells, for modulating production of a cytokine from AILIM-expressing cells, for inducing antibody-dependent cytocoxicity against AILIM-expressing cells and/or immune cytolysis or apoptosis of AILIM-expressing cells (I) is useful for treating or prophylaxis of delayed type allergy. (I) is useful for treating and prevention, and for inhibiting the cnset and/or advancement of the prophylaxis of delayed type allergy. (I) is useful for treating and prevention, and for inhibiting the cnset and/or advancement of the cheumacoid arthritis, multiple sclerosis, autoimmune thyroiditis, allergic contact-type dermatitis, chronic inflammatory dermatosis, sortamis, autoimmune or allergic disorders, inflammatory dermatosis, psoriasis, autoimmune or allergic disorders, inflammatory dermatosis, psoriasis, autoimmune or allergic disorders, inflammatory dermatosis, psoriasis, autoimmune or allergic disorders, inflammatory dermatosis, psoriasis, autoimmune or allergic disorders, inflammatory dermatosis, psoriasis, autoimmune or allergic disorders, inflammatory dermatosis, psoriasis, autoimmune or allergic disorders, inflammatory dermatosis, intestinal disorders such as ulcerative colitis, pneumonia, heparitis, and pancreative colitis, pneumonia, heparitis, and pancreative colitis, pneumonia, heparitis, and pancreative colitis, pneumonia, heparitis, and pancreative colitis, pneumonia, heparitis, and pancreative colitis, pneumonia, anti-human anti-human anti-human anti-human anti-human anti-human anti-human anti-human anti-human anti-human anti-human anti-human anti-human anti-human anti-human anti-human anti-human anti-human anti-human anti-human anti-human anti-hum
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New human monoclonal antibody that binds to activation inducible lymphocyte immunomodulatory molecule, useful for treating rheumatoid arthritis, multiple sclerosis and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human anti-tumour antigen antibody heavy chain variable region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 470;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 111 AVYYCAR--TYYYDSSGYYHDAFDIWGOGTMVTVSS 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 607; DB 5;
Pred. No. 7.5e-49;
9; Mismatches 16;
                                                                                                             Claim 30; Page 264-266; 300pp; English.
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76.3%;
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Matches 119;
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The present invention provides the coding and protein sequences for a number of human immune system associated proteins (HISABS). These can be used in the diagnosis and treatment of various autoimmune disorders, infections and cell proliferation diseases. The diseases include AIDS, adult respiratory distress syndrome, anaemia, asthma, atherosclerosis, crohn's disease, irritable bowel syndrome, multiple sclerosis, myasthenia gravis, osteoarthritis, rheumatoid arthritis, scleroderma, systemic lupus erythematosus, arteriosclerosis, cirrhosis and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and polynucleotides
or preventing immune
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                                                                                                                                                                                                                                                                                                                                                                            Length 236;
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                                                                               New human immune system associated proteins (HISAP) encoding the HISAP, useful for diagnosing, treating or cell proliferative disorders or infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AMYYCARADNYFDIVTG-YTSHYFDYWGRGTLVTVSS 156
                                                                                                                                                                                                                                                                                                                                                                            65.8%; Score 550.5; DB 4; 70.7%; Pred. No. 7.2e-44; tive 13; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human immunoglobulin variable heavy chain #2.
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                                                                                                                                                       Claim 1; Col 71-72; 54pp; English
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                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 70.7%
Matches 111; Conservative
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 Au-Young J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1995-006791/01.
N-PSDB; AAQ78940.
                                 WPI; 2001-030926/04.
                                                   N-PSDB; AAC66531
                                                                                                                                                                                                                                                                                                                                               Sequence 236 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9426895-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-NOV-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-MAR-2003
07-AUG-1995
 Hillman JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTSISTAYMELSRLTSDDT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YYMHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDT 110
                                                                                                                                                                                                                                                                                                                                                                              The present sequence is a human anti-tumour antigen monoclonal antibody (MAD) heavy chain variable region, useful in medicine, pharmacology and biochemistry. The isotype of a MAD secreted by the human/human hybridoma HT was determined to be mu and kappa. Human MAD was purified, and the antigen recognised by human MAD CLN"-IgM identified by western blotting
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps.
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                                                                                                                                                                                                                                                                                           Anticancer human monoclonal antibody variable region sequences - and related DNA and RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            system associated protein; HISAP-13; immune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Baughn MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |:|||| | AVYYCARGPK-----GYCSSTSCYFDYYYYGMDVWGQGTTV 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 AMYYCARADNYFDIVTGY---TSHYFDY-----WGRGTLV 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Guegler KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 586; DB 2;
Pred. No. 1.8e-47;
6; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human immune system associated protein HISAP-13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                infection; autoimmune disease; cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Corley NC,
                                                                                                                                                                                                                                                                                                                                                 Claim 3; Page 10; 14pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB36215 standard; protein; 236
/label= CDR_2
118. .139
/label= CDR_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70.0%;
Local Similarity 72.8%;
Les 118; Conservative (
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                                                                                                                                                                         95JP-00278266
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                                                                                                                                                                                                                                           WPI; 1997-276726/25.
N-PSDB; AAT75422.
                                                                                                                                                                                                            (HAGI/) HAGIWARA Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 146 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; immune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                       JP09100300-A
                                                                                                                                      03-OCT-1995;
                                                                                                                                                                           03-OCT-1995;
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                                                                                                         15-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                      Region
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Matches
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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                            Protein sequences (AAR66295-51) are novel human immunoglobulin heavy chain sequences encoded by novel isolated genes. The genes (AAR678339-7902) were isolated and cloned from a series of cosmid constructs: Y202; Y103; Y21; Y6;Y24; 3-31; M84, M118 and M131, by PCR amplification using primers AAQ78917-38. The genes are subdivided into 5 families of Vh genes. The fragments cover a region of 800 kb. The DNA fragments were isolated from high molecular weight DNA from human placenta. The DNA was partially digested with TaqI restriction enzyme. The fragments were sparated by gel electrophoresis and 35-45 kb fractions were collected. The fragments were ligated with clar-digested cosmid vector pJ881. The ligation products were in vitro packed and infected into E.coli 490A. The fragments were then subcloned by colony hybridisation. The VH by genes and the DNA fragments encoding them are useful in producing human immunoglobulin in mammalian hosts. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                               YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTSISTAYMELSRLTSDDT 120
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                                                                                                                                                                                                                                                                                                            Baughn MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, immunoglobulin, IGFAM-7, IGFAM, immune disorder, cancer, infection, inflammation, haematopoiesis, AIDS, allergy.
                                                                                                                                                                                                                                            Query Match 65.7%; Score 550; DB 2; Length 117; Best Local Similarity 83.5%; Pred. No. 3.5e-44; Matches 106; Conservative 4; Mismatches 7; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Guegler KJ, Gorgone GA,
 Disclosure, Page 32-33; 130pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .19
/label= signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY96295 standard; protein; 148 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= Ig_domain
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/label= IGFAM-7
34. .117
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98US-0113635P.
99US-0128194P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human IGFAM-7 immunoglobulin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-AUG-2000 (first entry)
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AVYYCAR 117
                                                                                                                                                                                                                                                                                                                                                                                                 AMYYCAR 127
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                                                                                                                                                                                                                          Sequence 117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200029583-A2
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07-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Domain
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The present sequence is the human immunoglobulin superfamily protein IGPAM-7. Its gene was isolated from a cDNA library of bladder tumour lissue. It is expressed in reproductive, gastrointestinal and immune and haematopoietic tissue, where cancer and inflammation are common. The gene, protein, its antibodies, agonists and antagonists are suitable for diagnosing and treating many diseases, including cancer, immune system disorders (such as inflammation, AIDS, allergies, anaemia, arteriosclerosis, asthma, atherosclerosis, cholecysticis, Crohn's arteriosclerosis, generalitus, emphysema, Graves' disease, hepatitis, multiple sclerosis, psoriasis, rheumatoid arthritis, scleroderma, systemic lupus erythematosus and ulcerative colitis), complications of cancer, heemodialysis and extracorporeal circulation, trauma and haematopoietic cancer (such as leukaemia) and infections caused by bacteria, viruses, fungi or parasites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20
                                                                                                                                               Immunoglobulin superfamily proteins, the agonist and antagonist of the protein is useful for preventing and treating disorders associated with altered levels of the protein such as cancer, immune system disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anti-TRAIL-R antibody related clone 0304 protein SEQ ID NO:29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65.4%; Score 547.5; DB 3;
68.6%; Pred. No. 7.9e-44;
iive 11; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 AMYYCARADNYFDIVTGYTSHYFDYWGRGTLVTVSS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               111 AIYYCARGD-----YGNSLDHWGOGNLVTVSS 137
<u>ن</u>
Yang
                                                                                                                                                                                                                                                                                       Claim 1; Page 83; 105pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABP57367 standard; protein; 145
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09-AUG-2001; 2001JP-00243040.
11-OCT-2001; 2001JP-00314489.
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Hillman JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-APR-2003 (first entry)
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Best Local Similarity 68.6°
Matches 107, Conservative
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                                                      WPI; 2000-387796/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antibody therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 148 AA;
                                                                                                  N-PSDB; AAA27387
   Lal P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200294880-A1.
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Synthetic.
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Lu DAM,
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The present invention describes antibodies or their functional fragments that bind to TRAIL-R1 and TRAIL-R2 antibodies have cytostatic and apoptotic activities, and can be used in antibody therapy. The antibodies can be applied as remedies and preventives of diseases due to cells expressing TRAIL-R1 and TRAIL-R2, which are useful in the therapy of malignant tumours. Remedies produced with the antibodies are highly safe, and avoid hepatotoxicity. The present sequence represents an anti-TRAIL-R antibody amino acid sequence from the
                                                                                  New anti-TRAIL-R antibodies with activity of inducing apoptosis of cancer cells and without exerting an effect on normal cells expressing TRAIL-Rs nor inducing injury to hepatocytes, for use in therapy of malignant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 YKINWVRQAPGQGLEWMGWMNPDTDSTGYPQKFQGRVTWTRNTSISTAYMELSSLRSEDT 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTSISTAYMELSRLTSDDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      identífication; cytostatic; cardioactive; neuroprotective; vulnerary; immunomodulatory; muscular; gynaecological; gastrointestinal; nephrotropic; antiinfective; antibacterial; gene therapy; wound; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; renal disorder; infectious disease; cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MDWTWRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    colon cancer; colon cancer antigen; diagnosis; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MDWTWRILFLVAAATSAHSQVQLVQSGAEMKKPGASVKVSCKTSGYTFTN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23;
                                                                                                                                                                                                                                                                                                                                                                                                                               DB 6; Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human colon cancer antigen protein sequence SEQ ID NO:1050.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AMYYCARADNYFDIVIGYTSHYFDY-----WGRGTLVTVSS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AVYYCARS-----YGSGSYYRDYYYGMDVWGQGTTVTVSS 145
                                                                                                                                                                                                                                                                                                                                                                                                                             65.1%; Score 544.5; DB 6; 67.3%; Pred. No. 1.5e-43; iive 14; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB53510 standard; protein; 146 AA
                                                                                                                                                                              Claim 54; Page 62; 92pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ruben SM;
                                  WPI; 2003-120790/11
Kataoka S;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 109; Conserv
                                                   N-PSDB; ABZ59698.
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 145 AA;
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Mori E,
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called human colon cancer antigens, given in AABS1234 to AABS4006. The human colon cancer antigens can have cytostatic, cardioactive, muscular, neuroprotective, immunomodulatory, gyraecological, gastrointestinal, vulnerary, nephrotropic, antiinfective and antibacterial activities, and can be used in gene therapy. The colon cancer antigen polymucleotides, or proteins and antibacies of the proteins are useful for the prevention, treatment and diagnosis of colon disorders, such as colon cancer. The polymucleotides may be used in diagnostics and research, such as for chromosome identification, and as hybridisation probes. The proteins may also be used to prevent diseases such as neural disorders, immune system disorders, wounds, renal disorders, reproductive disorders, immune system cardiovascular disorders, reproductive disorders, and and as hybridisation cardiorates and research and cardiovascular disorders. AAC98764 to AAC98772 and AABS4007 represent sequences used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antigen binding fragment 4B5; monoclonal antibody; cancer; neoplasm;
diagnosis; therapy; melanoma; neuroblastoma; glioma; sarcoma;
lung carcinoma; metastasis; anti-idiotype antibody; GD2 antigen; human.
                                             Colon cancer associated gene sequences, referred to as colon cancer antigens, useful for the treatment, prevention, and diagnosis of colon disorders such as colon cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MDWTWRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MDWTWRILFLVAAATSAHSQVQLVQSGAEVKKPGASVKVSCKASGYT-----FTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 AMYYCARADNY-----FDIVIGYISHYFDYWGRGTLVTV 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116 AVYYCARXRRWELLGMMWD------FDYWGQGTLVTV 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Monoclonal antibody 4B5 heavy chain variable region
                                                                                                                                                            to AAC98763 encode the human colon cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64.6%; Score 540.5; DB 3;
67.5%; Pred. No. 3.6e-43;
iive 12; Mismatches 15;
                                                                                                                        Claim 11; Page 1631; 2104pp; English.
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108; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-120769/10.
WPI; 2000-587534/55.
N-PSDB; AAC98267.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 146 AA;
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                                                                                                                                                          AAC97991
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Best Local (
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AAW88464
   임
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WO200202641-A1.

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This polypeptide comprises the heavy chain variable region of the recombinant human monoclonal antibody (MAD) 4B5. 4B5 recognises

C antibodies specific for GD2 antigen antibodies. Antibodies specific for GD2 antigen antibodies generationa, cancers including glioblastoma, neuroblastoma, compared and/or metastatic melanoma, breast adenocarcinoma, lung carcinoma, colon adenocarcinoma and denocarcinoma. The invention encompasses 4B5 derivatives with immunologic specificity for antibodies specific for GD2. These control immunologic specificity for antibodies specific for GD2. These control immunologic specificity for antibodies specific for GD2. These control immunologic specificity for antibodies specific of GD2. These include control immunologic specificity for antibodies specific for GD2. These include control immunologic specific for antibodies specific for antibodies specific for GD2. These include control immunologic specific for antibodies specific for antibodis specific for GD2. These includes control for antibodies for specific for GD2 and includes for specific for GD2. These for antibody vegtons are also provided, and therapeutic plasmids and vectors, including vaccinia virus vectors, comprising these control control control control control or specific for GD2, and is particularly control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control co
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVŢMSRDTSISTAYMELSRLTSDDŢ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MDWTWRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MDWTWRVLFLVAAATSARSQVQLVQSGAEVKKPGASVKVSCKASGYT-----FTS 50
                                                  antibody 4B5 polynucleotides and polypeptides - used to develop
fucts for the diagnosis and treatment of cancers and for prophylactic
rapy to reduce risk of recurrence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64.5%; Score 540; DB 2; Length 476; 68.6%; Pred. No. 1.6e-42; ive 14; Mismatches 20; Indels :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AMYYCAR-ADNYFDIVTGYTSHYF--DYWGRGTLVTVSS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |:|:||||||||:
|111 AVYFCARNADN---VEMAAIYHYYGMDVWGQGTTVTVSS 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human BLyS binding scFv SEQ ID 1722.
                                                                                                                                                       Claim 1; Page 79-80; 83pp; English.
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This invention describes novel antibodies that immunospecifically bind to be Lymphocyte Stimulator (BLyS) polypeptides. BlyS is a member of the tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunoadulatory, antirheumatic and antiAnDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant ElyS expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatodia arthritis, immunodeficiency (CVID) propression
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                                                                                                                                                                                                                                                                                                                                                              Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 OVOLOOSGAEVKKPGASVKVSCKASGYTFTG------YYMHWVRQAPGQGLEWMGW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64.4%; Score 539; DB 5; Length 250; ilarity 75.9%; Pred. No. 9.4e-43; Conservative 10; Mismatches 13; Indel8
                                                                                                                                                                                                                                                                                        Choi GH, Vaughan T, Hilbert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human monoclonal antibody against CTGF SEQ ID NO:8.
                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 2457-2458; 3148pp; English.
                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC. (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
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                                                                                                                                      17-OCT-2000; 2000US-0240B1EP.
16-MAR-2001; 2001US-0276246P.
21-MAR-2001; 2001US-0277379P.
25-MAY-2001; 2001US-0293499P.
                                                                                     15-JUN-2001; 2001WO-US019110.
                                                                                                                          2000US-0212210P.
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                                                                                                                                                                                                                                                                                        Ruben SM, Barash SC,
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Matches 104; Conserv
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16-APR-2001; 2001WO-US008656.
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                                                                                                                                                                                                      Nucleic acids encoding a vaccination, testing and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 68.8
Matches 108; Conservative
                                                                                                                                                                      WPI; 2001-611725/70.
                                                                                                     (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunosuppressive.
                                                                                                                                      Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 746 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAX30020 to AAX90029 encode monoclonal antibodies which react with human connective tissue growth factor (CTGP). AAX24369 to AAX24378 represent these monoclonal antibodies. The antibodies are useful in the diagnosis, prevention and treatment of cell proliferation disorders in which CTGF is, implicated, including fibrosis of lung, Kidney, liver and other tissues; liver cirrhosis, nephritis, skin ulcers and keloid, rheumatoid arthritis; rheumatic vascular inflammation; hepatitis, and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTSISTAYMELSRLTSDDT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52 XYMHWVRQAPQQGLEWMGWINPNSSGTHYAQMFQGRVTVTRDTSISTAYMELSRLRSDDT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MDWTWRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MDWTWRISFLVAAATGAHSOVOLVOSGAEVKKPGASVKVSCKAFWL------HLSPG 51
                                                                                                                                                                                                                                                                                                                                                                   New monoclonal antibody reactive with connective tissue growth factor useful in the treatment of cell proliferation disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; vaccination; gene therapy; nutritional supplement;
stem cell proliferation; haematopoiesis; nerve tissue regeneration;
immune suppression; immune stimulation; anti-inflammatory; leukaemia.
cell proliferation disorder; fibrosis; liver cirrhosis; nephritis; skin ulcer; keloid; rheumatoid arthritis; hepatitis; cancer; rheumatic vascular inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63.6%; Score 532; DB 2; Length 149; llarity 68.6%; Pred. No. 2.3e-42; Conservative 9; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 AMYYCARADNYFDIVTGYTSHYFDYWGRGTLVTVSS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |:|||||
| SVYYCAR----EGIAAAAIYGMDVWGQGTTVTVSS 142
                                                                                                                                                                                                                                                                                     Takigawa M;
                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 17; Page 177-178; 212pp; Japanese.
                                                                                                                                                                                                                                                                                     Sakamoto S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human secreted protein #2295.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU31804 standard; protein; 746 AA.
                                                                                                                                                                   98WO-JP005697
                                                                                                                                                                                                   97JP-00367699.
                                                                                                                                                                                                                                                 (NISB ) JAPAN TOBACCO INC
                                                                                                                                                                                                                                                                                   Tezuka K,
                                                                                                                                                                                                                                                                                                                     WPI; 1999-430232/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
es 107; Conserv
                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAX90021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 149 AA;
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                                                                                                                                                               16-DEC-1998;
                                                                 Homo sapiens
                                                                                                 W09933878-A1
                                                                                                                                                                                                 25-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                   15-DEC-1998;
                                                                                                                                                                                                                                                                                     Pamatani T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-DEC-2001
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Matches

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RESULT 14 AAU31804

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The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation, to regulate haematopoiesis, and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or AMUSSHOL-AMUSSHOL-AMUSSHOL-AMUSAN represent the amino acid sequences of novel human secreted proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 YSVHWVRQAPGCGLEWMGRINPNSGATDYAHKFQGRVTMSRDTSISTAYMELSRLTSDDT 120
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                                                                                                                                                                                                                                                                                                                              range of human polypeptides, useful in genetic therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MDWTWRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Humanised; anti-Fas antibody; mouse hybridoma; autoimmune disease; diagnosis; CDR; complementarity determining region; apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 746;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 529.5; DB 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 20; Page 511; 765pp; English.
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18-APR-2000; 2000US-00552929.
26-JAN-2001; 2001US-00770160.
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98JP-00204318.

03-JUL-1998;

18-JAN-2000.

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The present invention describes a recombinant antibody (A) which binds to fas antigen, and controls and induces apoptosis in cells which expressed fas antigen. The complementarity determining regions (CDR) of (A) contain amino acid sequences obtained from a mammal other than human, other regions contain amino acid sequences from human and they partly contain modified amino acids. A) has immunosuppressive activity, (A) is used for treating and/or diagnosing autoimmune diseases. The present sequence represents a specifically claimed heavy chain variable region of (A)
                                                                                                                                                                                                   Novel recombinant antibody used for treating and diagnosing autoimmune diseases - is humanized anti-Fas antibody which controls and induces apoptosis in cells expressing fas antigen.
                                                                                                                       (IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK.
                                                                                                                                                                                                                                                                                 Claim 13; Page 13; 25pp; Japanese.
                                                                                98JP-00204318
                                                                                                                                                              WPI; 2000-199626/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 135 AA;
                                                                                03-JUL-1998;
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м . 61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDISISTAYWELSRLTSDDT 120 1 MDWTWRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA 60 23; Gaps 63.1%; Score 528.5; DB 3; Length 135; 66.9%; Pred. No. 4.4e-42; tive 12; Mismatches 17; Indels 23 121 AMYXCARADNYFDIVTGYTSHY-FDYWGRGTLVTVSS 156 Best Local Similarity 66.9% Matches 105; Conservative Query Match ò ઠ Бb g à g

5, 2004, 13:24:17 Search completed: April Job time: 51.4162 secs

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Sequence 6, Appli
Sequence 18, Appl
Sequence 1050, Ap
Sequence 3, Appli
Sequence 3, Appli
Sequence 172, Ap
Sequence 172, Ap
Sequence 172, Ap
Sequence 12, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 1640, Appl
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Sequence 10, Appl
                                                                                                                                                                  April 5, 2004, 13:42:12; Search time 36.6904 Seconds (without alignments) 1116.513 Million cell updates/sec
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1: \cgn2_6/ptodata/2/pubpaa/USO7_PUBCCMB.pep:*
2: \cgn2_6/ptodata/2/pubpaa/RCT_May PUB.pep:*
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12: \cgn2_6/ptodata/2/pubpaa/USO0_PUBCCMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-925-299-1050
US-09-925-299-1050
US-09-747-669-3
US-09-747-669-3
US-09-88-1722
US-10-390-986-12
US-10-390-986-12
US-09-880-748-1723
US-10-390-986-12
US-09-880-748-1640
US-09-880-748-1640
US-09-880-748-1640
US-09-880-748-1640
US-09-890-986-46
US-09-269-921-123
US-09-269-921-123
US-10-310-398-46
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Maximum Match 100%
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ALIGNMENTS

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RESULT 1

SECULT 1

SEQUENCE 6, Application US/10044569B

Sequence 6, Application US/10044569B

Sequence 6, Application US/2030175268A1

Sequence 6, Application No. US20030175268A1

GENERAL INFORMATION:
APPLICANT: Saint-Read and pharmaceutical composition for preventing and the price of INVENTION: Method and pharmaceutical composition for preventing TITLE OF INVENTION: Method and pharmaceutical composition for preventing TITLE OF INVENTION: Method and pharmaceutical composition for preventing TITLE OF INVENTION: Method and pharmaceutical composition for preventing TITLE OF INVENTION: MOMBER: US 60/261,405

PRIOR FPLING DATE: 2002-01-11

NUMBER OF FEQ ID NOS: 8

SEQ ID NOS: 8

SEQ ID NO 6

TENGTH: 156

TYPE: PRT

OGGANISM: Home sapiens

FEATURE:
NAME/KEY misc_feature

LOCATION: (132)...(132)

OTHER INFORMATION: complementary determining region number two FEATURE:

NAME/KEY: misc_feature

LOCATION: (332)...(435)

OTHER INFORMATION: complementary determining region number three LOCATION: (332)...(435)

OTHER INFORMATION: complementary determining region number three LOCATION: (332)...(435)

OTHER INFORMATION: complementary determining region number three LOCATION: (332)...(435)

OTHER INFORMATION: complementary determining region number three LOCATION: (332)...(435)

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OTHER INFORMATION: complementary determining region number three US-10-044-569B-6

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OTHER INFORMATION: complementary determining region number three US-10-044-569B-6

OTHER INFORMATION: complementary determining region number on US-10-044-569B-6

OTHER INFORMATION: complementary determining region number on US-10-044-569B-6

OTHER INFORMATION: complementary determining region number on US-10-044-569B-6

OTHER INF
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SEQ ID NO 1050
LENGTH: 146
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                    FEATURE:
NAME/KEY: SITE
LOCATION: (123)
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Fatent No. US2002012658A1
GENERAL INFORMATION:
APPLICANT: TSUJi, Takashi
TITLE OF INVENTION:
TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE ALLIM AND
TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
TITLE OF INVENTION UNMER: US 2001-99508
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2000-05-18
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                     61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKRQGRVTMSRDTSISTAYMELSRLTSDDT 120
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                                                                 1 MDWTWRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA
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Fatent No. US20020055627A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INFORMATION: Nucleic Acids, Proteins and Antibodies
FILE REPERENCE: PA10.2
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1099-03-12
NUMBER: OF SEQ ID NOS: 1556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 72.5%; Score 607; DB 9; Length 470; Best Local Similarity 76.3%; Pred. No. 7.8e-52; Matches 119; Conservative 9; Mismatches 16; Indels
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US-09-859-053-28
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NAME/KEY: SITE

LOCATION: (123)

CTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-09-925-299-1050
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) OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-925-299-1050
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                                                                                                                                              25;
                                                                                      Length 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1050, Application US/09925299;
Sequence 1050, Application US/09925299;
Publication No. US20030040617A9;
GENERAL INPORMATION:
ITILE OF INVENTION: Nucleic Acids, Proteins and Antibodies;
FILE REPERRENCE: PA102
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT APPLICATION NUMBER: DO1-08-10
PRIOR PILING DATE: 2000-09-10
PRIOR PILING DATE: 2000-09-10
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: Patentin Ver. 2.0
FEMBLY APPLICATION VER. 1000-126
SOFTWARE: Patentin Ver. 2.0
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64.6%; Score 540.5; DB 10; Length :
Best Local Similarity 67.5%; Pred. No. 8e-46;
Matches 108; Conservative 12; Mismatches 15; Indels
                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                            121 AMYYCARADNY-----FDIVTGYTSHYFDYWGRGTLVTV 154
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                                                                                Query Match
64.6%; Score 540.5; DB 9;
Best Local Similarity 67.5%; Pred. No. 8e-46;
Matches 108; Conservative 12; Mismatches 15;
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ORGANISM: Homo sapiens
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APPLICANT: Johan Tobacco, Inc.
TITLE OF INVENTION: Monoclonal Antibody Against Connective Tissue Growth Factor TITLE OF INVENTION: and Medicinal Uses Thereof
FILE REFERENCE: J1-009PCT
CURRENT APPLICATION NUMBER: US/10/390,986
CURRENT FILING DATE: 2003-03-17
PRIOR APPLICATION NUMBER: US/9/582,337
PRIOR APPLICATION NUMBER: US/9/582,337
PRIOR APPLICATION NUMBER: JP 91997-367699
                                                                                                                                                                                                                                                                     61 YSVHWVRQAPGOGLEWMGRINPNSGATDYAHKFQGRVTMSRDTSISTAYMELSRLTSDDT 120
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                                                                                                20 QVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTAYSVHWVRQAPGQGLEWMGR
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                                             1 MDWTWRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA
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APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-15

PRIOR PLIOR DATE: 2000-10-17

PRIOR PLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2001-03-16

PRIOR PLICATION NUMBER: 60/277,379

PRIOR PLILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR PLICATION NUMBER: 60/293,499

PRIOR PLILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: PATENTIN VET: 2:0

SEQ ID NO 1722

LENGTH: 250
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64.4%; Score 539; DB 10;
Best Local Similarity 75.9%; Pred. No. 2.1e-45;
Matches 104; Conservative 10; Mismatches 13
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Publication No. US20030059937A1
GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-09-880-748-1722
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US-10-390-986-8
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             GENERAL INFORMATION:

APPLICANT: Dan, Michael D.

APPLICANT: Dan, Michael D.

APPLICANT: Dan, Michael D.

APPLICANT: Balbh, Manscor

ITILE OF INVENTION: ANTIGEN BINDING FRAGMENTS, DESIGNATED

TITLE OF INVENTION: AND DETECTION OF CANCER CELLS, NUCLEOTIDES

ITILE OF INVENTION: AND DETECTION OF CANCERS

ITILE OF INVENTION: AND DETECTION OF CANCERS

ITILE OF INVENTION: AND DETECTION OF CANCERS

FILE REFERENCE: 316082001001

CURRENT APPLICATION NUMBER: US/09/747,669

PRIOR TELING DATE: 1998-07-07

NUMBER: OF SEQ ID NOS: 7

SOFTWARE FEASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER 
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SQUENCE 3, Application US/10290703

Publication No. US2030118593A1

GENERAL INPORMATION:

APPLICANT: Dan, Michael D.

APPLICANT: Dan, Michael D.

APPLICANT: Dan, Michael D.

TITLE OF INVENTION: ABTIGEN BINDING FRAGMENTS, DESIGNATED

TITLE OF INVENTION: ABTIGEN BINDING FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS

TITLE OF INVENTION: ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS

TITLE OF INVENTION: ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS

TITLE OF INVENTION: ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS

TITLE OF INVENTION: ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS

TITLE OF INVENTION: ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS

TITLE OF INVENTION NUMBER: US 99/147,669

PRIOR FILING DATE: 1994-07-07

PRIOR FILING DATE: 1997-07-08

NUMBER OF SEQ ID NOS: 7

SOFTWARE: FASTSEQ for Windows Version 4.0

SEC IN NO 3

LENGTH: 476

TYPE: PRT

TYPE: PRT

TYPE: PRT

TYPE: PRT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 64.5%; Score 540; DB 9; Length 476; Best Local Similarity 68.6%; Pred. No. 3.5e-45; Matches 109; Conservative 14; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 AMYYCAR-ADNYFDIVTGYTSHYF--DYWGRGTLVTVSS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Synthetic construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
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Best Local Similarity 68.6%
Matches 109; Conservative
US20020122807A1
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US-10-290-703-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-747-669-3
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Query Match
Best Local Similarity 67.3%;
Matches 105; Conservative
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ORGANISM: Homo sapiens
US-09-880-748-1640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens
US-10-390-986-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTSISTAYMELSRLTSDDT 120
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                                                                                                                                                                                                                                                                                                                                                                                                  1 MDWTWRISFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKAFWL-----HLSPG 51
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Fublication No. US2003005993741

GENERAL INFORMATION:

TITLE OF INVESTION: Antibodies that Immunospecifically Bind BLyS

CURRENT RILING DATE: 2000-06-15

CURRENT FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-16

PRIOR FILING DATE: 2000-06-16

PRIOR PRILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-22

PRIOR FILING DATE: 2001-03-25

NUMBER OF SEQ ID NOS: 2329
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                                                                                                                                                                                                                                                          63.6%; Score 532; DB 14; Length 149; 68.6%; Pred. No. 5.7e-45; ive 9; Mismatches 26; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112 AVYYCAR----EGIAAAAIYGMDVWGQGTTVTVSS 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 AMYYCARADNYFDIVTGYTSHYFDYWGRGTLVTVSS 156
                             P1998-356183
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PRIOR APPLICATION NUMBER: JP P19
PRIOR FILING DATE: 1998-12-15
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
LENDH: 149
TYPE: PRT
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SEQ ID NO 1723
LENGTH: 250
                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 68.67
Matches 107; Conservative
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US-09-880-748-1723
                                                                                                                                                                                       , ORGANISM: Homo sapiens
US-10-390-986-8
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US-09-880-748-1640

Sequence 1640, Application US/09880748

Publication NO. US20030059937A1

GENERAL INFORMATION:

APPLICATION OF ALLIANCE THAT INMUNOSPECIFICALLY RUBEN C. ALLIANCE THAT INCOMPATION:

FILE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT APPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-10-17

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR PRILING DATE: 2001-03-21

PRIOR PRILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239

SEQ ID NOS: 3239

SEQ ID NO 1640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 525.5; DB 14; Length 146;
Pred. No. 2.5e-44;
9; Mismatches 25; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62.8%; Score 525.5; DB 10; Length 256; ilarity 74.3%; Pred. No. 4.7e-44; Conservative 9; Mismatches 15; Indels 13;
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Matches 104; Conserv
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OTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence OTHER INFORMATION: of reshaped human anti-HM 1.24 antibody H chain V region OTHER INFORMATION: version p
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                                                                                                                                                                                                                               FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Humanized H chain OTHER INFORMATION: region (version p) of anti-HM1.24 antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MDWTWRILFLVAAATGAHSQVQLVQSGAEVXKPGASVKVSCKTSGYNFTGYSASGHIFTA
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Publication No. US20030129185A1

GENERAL INFORMATION:
APPLICANT: Onc. Noichiro
APPLICANT: Onc. Noichiro
APPLICANT: Onc. Noichiro
APPLICANT: Tsuchiya, Masayuki
APPLICANT: Tsuchiya, Masayuki
APPLICANT: Tsuchiya, Masayuki
APPLICANT: Tsuchiya, Masayuki
APPLICANT: Tsuchiya, Masayuki
APPLICANT: Noichihara, Yasushi
APPLICANT: Noichihara, Yasushi
APPLICANT: Noichihara, Yasushi
APPLICANT: Noichihara, Yasushi
PRICAN APPLICATION NUMBER: US/10/218,253
CURRENT FILING DATE: 1999-04-01
PRIOR PILING DATE: 1999-04-01
PRIOR PLILING DATE: 1999-10-03
PRIOR PILING DATE: 1999-10-03
PRIOR PILING DATE: 1999-10-04

PRIOR PILING DATE: 1999-10-04

PRIOR PILING DATE: 1999-10-04

PRIOR PILING DATE: 1996-10-04

SOFTWARE: PAECHLIN VONSE: 137

SOFTWARE: PAECHLIN Ver. 2.0

SOFTWARE: PAECHLIN Ver. 2.0
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Best Local Similarity 66.7%; Pred. No. 3.7e-44;
Matches 104; Conservative 11; Mismatches 24
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Best Local Similarity 66.7%; Pred. No. 3.7e-44;
Matches 104; Conservative 11; Mismatches 24
PRIOR APPLICATION NUMBER: JP 9-
PRIOR FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 203
SOFTWARE: PatentIN Ver. 2.1
SEQ ID NO 46
LENGTH: 139
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                                                                                                                                                                        TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                       US-09-509-098-46
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                                                                                                                                                                           51 INPNSGGTNYAQKFQGW/TMTRDTSISTAYMELSSLRSEDTAVYYCARARGSYDILIGYY 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFOGRVTMSRDTSISTAYMELSRLTSDDT 120
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                                                                                                                                            80 INPNSGATDYAHKFQGRVTMSRDTSISTAYMELSRLTSDDTAMYYCARADNYFDIVTGY- 138
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                                                                                  1 OVOLVOSGAEVKKPGSSVKVSCKASGYTFTG-----YYMHWVRQAPGQGLEWMGW 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 123. Application US/09269921
| Sequence 123. Application US/09269921
| Publication No. US20030045691A1
| GENERAL INFORMATION
| APPLICANT: One, Voichiro
| APPLICANT: Tucchiya, Masayuki
| APPLICANT: Tucchiya, Masayuki
| APPLICANT: Yoshimara, Yasushi
| APPLICANT: Koishimara, Yasushi
| TILEL OF INVENTION: RESHAPED HUMAN ANTI-HM 1.24 ANTIBODY
| TILE OF INVENTION INVERS: US/09/269,921
| CURRENT PILING DATE: 1999-04-01
| BARLIER PILING DATE: 1999-04-01
| BARLIER PILING DATE: 1997-10-03
| BARLIER FILING DATE: 1997-10-03
| BARLIER FILING DATE: 1996-10-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 62.5%; Score 523.5; DB 10; Length
Best Local Similarity 66.7%; Pred. No. 3.7e-44;
Matches 104; Conservative 11; Mismatches 24; Indels
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US-09-509-08-46
Squence 46, Application US/09509098
Publication No. US2003103970A1
GENERAL INFORMATION:
TITLE OF INVENTION: NATURAL HUMANIZED ANTIBODY
TITLE OF INVENTION: NATURAL HUMANIZED ANTIBODY
CURRENT APPLICATION NUMBER: US/09/509,098
CURRENT FILING DATE: 2000-03-22
PRIOR FILING DATE: 1998-10-02
                                                                                                                                                                                                                                                          139 --TSHYFDYWGRGTLVTVSS 156
                                                                                                                                                                                                                                                                                            111 RPGDGYFDYWGRGTLVTVSS 130
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SEQ ID NO 123
LENGTH: 139
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RESULT 15

US-10-390-96-10

S-10-390-96-10

SUBJICATION NO. US20030166011A1

GENERAL INFORMATION:

APPLICANT: USPAINTON:

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

CURRENT APPLICATION NUMBER: US/10/390,986

FILE REFERENCE: J-009PCT

CURRENT PILING DATE: 2003-03-17

PRIOR PILING DATE: 1997-12-25

PRIOR FILING DATE: 1997-12-25

PRIOR APPLICATION NUMBER: US/97-367699

PRIOR FILING DATE: 1998-12-15

PRIOR APPLICATION NUMBER: US/97-367699

PRIOR FILING DATE: 1998-12-15

SOFTWARE: PATENTING USE: 2000-06-23

SEQ ID NO:

SEQ ID NO:

TYPE: PATENTING USE: 2000-06-23

TYPE: PATENTING USE: 2000-06-23

TYPE: PATENTING USE: 2000-06-23

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TYPE: PAT
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Best Local Similarity 67.3%; Pred. No. 3.9e-44;
Matches 105; Conservative 9; Mismatches 25; Indels 17; Gaps
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                                                     ORGANISM: Homo sapiens
US-10-390-986-10
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Search completed: April 5, 2004, 13:59:14 Job time : 37.6904 secs

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Sequence 8, Appli
Sequence 12, Appl
Sequence 28, Appl
Sequence 10, Appl
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2, App
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Sequence 112, App
Sequence 38, Appl
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Sequence 90, Appl
                                                                                           (without alignments)
575.678 Million cell updates/sec
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837
1 MDWTWRILFLVAAATGAHSQ.......GYTSHYFDYWGRGTLVTVSS 156
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Sequence 10
Sequence 10
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Sequence 4
Sequence 9
Sequence 1
Sequence 1
Sequence 1
                                                                             April 5, 2004, 13:36:42 ; Search time 13.9898 Seconds
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/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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US-00-582-337-12
US-00-582-337-12
US-08-137-1170-112
US-08-137-1170-112
US-08-513-968-33
US-08-513-968-34
US-08-513-968-94
US-08-477-878-94
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US-08-137-117-100
US-08-51-2117-100
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US-08-51-2117-100
US-08-51-2117-100
US-08-51-2117-100
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Maximum Match 100%
Listing first 45 summaries
                                                   OM protein - protein search, using sw model
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Maximum DB seq length: 2000000000
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Perfect score:
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Sednence	Seguence	Sednence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	equenc	Sequence	Seguence	Sequence	Sequence	Seguence	Sequence	
-08-12/-/21A-1 -08-485-246A-1	US-08-476-176B-16	-08-1	US-08-485-246A-16	US-08-836-561-63	US-09-434-122-63	US-08-476-176B-12	US-08-127-721A-12	US-08-485-246A-12	US-08-545-809A-128	US-08-646-265A-99	US-08-217-918-4	US-08-579-378A-12	PCT-US93-11612-12	US-08-253-877C-19	US-08-452-164A-19	US-08-603-024-18	
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ALIGNMENTS

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Sequence 13, Application US/09049672A

Sequence 13, Application US/09049672A

Patent No. 6135941

Sequence 13, Application US/09049672A

Sequence 13, Application US/09049672A

Sequence 13, Application US/09049672A

APPLICANT: Lai, Preeti

APPLICANT: Tang, Y. Tom

APPLICANT: Tang, Y. Tom

APPLICANT: Guegler, Karl J.

APPLICANT: Guegler, Karl J.

APPLICANT: Guegler, Karl R.

APPLICANT: Guegler, Karl R.

APPLICANT: Guegler, Karl R.

APPLICANT: Guegler, Karl R.

APPLICANT: Guegler, Karl R.

APPLICANT: Guegler, Karl R.

APPLICANT: USA

STREET: 31404 Porter Drive

CONDYTER: Tan Compatible

CONDYTER: Tan Compatible

CONDYTER: Tang Compatible

CONDYTER: Tang Compatible

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CONDYTER: Tang Compatible

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CONDYTER: Tang Compatible

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CONDYTER: Tang Compatible

CONDYTER: Tang Compatible

TELECOMMUNICATION NUMBER: 39,132

REGISTRATION NUMBER: 39,132

REGISTRATION NUMBER: 39,132

REGISTRATION NUMBER: 39,132

REGISTRATION NUMBER: 39,132

REGISTRATION NUMBER: 39,132

REGISTRATION NUMBER: 39,132

REGISTRATION NUMBER: 39,132

REGISTRATION OF SEQ ID NO: 13: SEQUENCE CHARACTERISTICS: LENGTRATE TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER: TANGER
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SYNONOTO1

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US-09-582-337-12

Sequence 12, Application US/09582337

Patent No. 6562618

Sequence 12, Application US/09582337

Sequence 12, Application US/09582337

Patent No. 6562618

PAPLICANT: Japan Tobacco, Inc.

APPLICANT: Japan Tobacco, Inc.

APPLICANT: Japan Tobacco, Inc.

APPLICANT: Japan Tobacco, Inc.

APPLICANT: Japan Tobacco, Inc.

APPLICANTION: And Medicinal Uses Thereof

CURRENT APPLICATION NUMBER: US/09/582,337

CURRENT FILING DATE: 1997-12-25

PRIOR PILING DATE: 1998-12-15

PRIOR FILING DATE: 1998-12-15

SOUTWARE: PATENTION OF SEQ ID NOS: 27

SEQ ID NO 12

LENGTH: 146

LENGTH: 146
                                                                                                                                                                                                                                                                                                                  APPLICANT: Japan Tobacco, Inc.

APPLICANT: Japan Tobacco, Inc.

TITLE OF INVENTION: Monoclonal Antibody Against Connective Tissue Growth Factor TITLE OF INVENTION: Monoclonal Uses Thereof FILE REFERENCE: J1-009PCT

CURRENY APPLICATION NUMBER: US 9509/582,337

CURRENY FILING DATE: 2000-06-23

PRIOR APPLICATION NUMBER: JP P1997-367699

PRIOR APPLICATION NUMBER: JP P1997-356183

PRIOR APPLICATION NUMBER: JP P1998-356183

PRIOR FILING DATE: 1998-12-15

SOFTWARE: PATCHIN VOR: 2.0

SEQ ID NOS: 27

SOFTWARE: PATCHIN VOR: 2.0
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Pred. No. 5.7e-47;
9; Mismatches 26; Indels
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| 12 AVYYCAR-----EGIAAAAIYGMDVWGQGTIVTVSS 142
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                                                                                                                                                                                                                                              Sequence 8, Application US/09582337; Patent No. 6562618; GENERAL INFORMATION:
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Best Local Similarity 68.6%;
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
US-09-582-337-8
                                                                                                                            111 AVYYCAR 117
                                                                             121 AMYYCAR 127
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Best Local Similarity
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US-09-582-337-12
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TYPE: PRT
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DS-918-945-904-90

DS-918-945-904-90

Sequence 90, Application US/08545809A

Patent No. 6096878

GENERAL INFORMATION: Tasuku

APPLICANT: Honjo, Tasuku

APPLICANT: Honjo, Tasuku

APPLICANT: Honjo, Tasuku

APPLICANT: Honjo, Tasuku

APPLICANT: Honjo, Tasuku

TITLE 0F INVENTION: HUMAN IMMUNOGLOBULIN VH GENE

TITLE 0F INVENTION: HUMAN IMMUNOGLOBULIN VH GENE

TITLE 0F INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME

NUMBER OF SEGMENTS: 145

CONTAIN: US

CONTAIN: US

CONTAIN: US

COMPUTER: Each Sector

STATE: MA

COMPUTER: IBM Compatible

COMPUTER: IBM Compatible

COMPUTER: SeatsEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/JP93/00603

FILING DATE: 10-MAY-1993

FILING DATE: 10-MAY-1993

FILING DATE: 10-MAY-1993

FILING DATE: 10-MAY-1993

FILING DATE: 10-MAY-1993

FILING DATE: 10-MAY-1993

FILING DATE: 10-MAY-1993

FILING DATE: 10-MAY-1993

FELENDAME FREENCE/DOCKET UNFORMATION:

NAME: Freenan, John W.

REFERENCE/DOCKET UNFORMATION:

TELEBHONE: 617-642-8906

TELEBHONE: 617-642-8906

TELEBHONE: 617-642-8906
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                                                                                                                               19;
                                                                                  Length 236;
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                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                       121 AMYYCARADNYFDIVTG-YTSHYFDYWGRGTLVTVSS 156
                                                                                  DB 3;
                                                                             65.8%; Score 550.5; DB 3 70.7%; Pred. No. 1.3e-48; iive 13; Mismatches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 200154
INFORMATION FOR SEQ ID NO: 90:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
                                                                             Query Match
Best Local Similarity 70.7%
Matches 111; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
            ; CLONE: 3551457
US-09-049-672A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-545-809A-90
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Sequence 10, Application US/09582337
Sequence 10, Application US/09582337
Patent No. 6562618
GENERAL INFORMATION:
TOTAL OF INVENTION: Monoclonal Antibody Against Connective Tissue Growth Factor:
TITLE OF INVENTION: Monoclonal Insert Thereof
FILE REFERRING: J1-009PCT
CURRENT APPLICATION NUMBER: US/09/582,337
CURRENT APPLICATION NUMBER: US P1997-367699
PRIOR FILING DATE: 1997-12-25
PRIOR FILING DATE: 1998-12-15
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PATENTION OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
LENGTH: 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51 HWMHWVRQAPGQGLEWVGEFNPSNGRTNYNEKFKSRVTMTLDTSTNTAYMELSSLRSEDT 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTSISTAYMELSRLTSDDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 62.5%; Score 523.5; DB 4; Best Local Similarity 67.3%; Pred. No. 4.1e-46; Matches 105; Conservative 9; Mismatches 25;
                                                                       121 AMYYCARADNYFDIVTGYTSHYFDYWGRGTLVTVSS 156
                                                                                                                                        111 AVYYCASRD--YD----YDGRYFDYWGQGTLVTVSS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 AMYYCARADNYFDIVTGYTSHYFDYWGRGTLVTVSS 156
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
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Patent No. 5795965
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
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COUNTRY: USA
ZIP: 2007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens
US-09-582-337-10
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OPERATING SYSTEM:
SOFTWARE: PatentI
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US-08-137-117D-112
                                                                                                                                                                                                                                                                                -09-582-337-10
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                                                                                                                                                                                                                                                         *SVHWVRQAPGGGLEWMGRINPNSGATDYAHKFQGRVTWSRDTSISTAYMELSRLTSDDT 120
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                                                                                                                                               ----LTE 50
                                                                       1 MDWTWRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA
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                                                                                                                                           1 MDCTWRIFFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYT---
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       25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Bendig, Mary M.
APPLICANT: Retleborough, Catherine A.
APPLICANT: Standand, Jose
APPLICANT: Standand, Jose
TITLE OF INVENTION: Humanized and Chimeric Monoclonal
TITLE OF INVENTION: Antibodies
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Boulevard, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/946,421
FILING DATE: 06-NOV-1992
CLASSIFICATION 7424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP92/00480
FILING DATE: 04-MAR-1992
PRIOR APPLICATION NUMBER: WO PCT/EP92/00480
FILING DATE: 06-MAR-1991
ATTONNEY/AGENT INPORMATION:
NAME: Hamlet-King, Datas
REGISTRATION NUMBER: 33,302
                                                                                                                                                                                                                                                                                                                                                           121 AMYYCARADNYFDIVTGYTSHYFDYWGRGTLVTVSS 156
                                                                                                                                                                                                                                                                                                                                                                                                                               111 AVYYCATS-----TVVTPWYFDYWGQGTLVTVSS 139
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62.7%; Score 525; DB 1;
Best Local Similarity 64.7%; Pred. No. 2.8e-46;
Matches 101; Conservative 17; Mismatches 22
       9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 2200 Clarendon Boulevard, s
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OMPOTTER: IBM PC compatible
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Patent No. 5558864
GENERAL INFORMATION:
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REFERENCE/DOCKET NUMBER: MEX
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 26
SEQUENCE CHARACTERICTICS:
LENGTH: 140 amino acids
TYPE: amino acid
TYPE: amino acid
       105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE:
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       Matches
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61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTSISTAYMELSRLTSDDT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: MAEDA, Hiroaki
APPLICANT: MAEDA, Hiroaki
APPLICANT: MAKIZUMI, Keiichi
APPLICANT: SHOGAKI, Koiichi
APPLICANT: SHOGAKI, Koiichi
APPLICANT: GHOGAKI, Kazuhiko
APPLICANT: KIMACHI, Hirofumi
APPLICANT: TOKIYOSHI, Hirofumi
APPLICANT: TOKIYOSHI, Sachio
TITLE OF INVENTION: ANTI-HIV MONOCLONAL ANTIBODY
NUMBER OF SEQUENCES: 86
CORRESPED: BROWNY ****
STRPPT
STRPPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 AMYYCARADNYFDIVTGYTSHYFDYWGRGTLVTVSS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .6e-46
                                               APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA: APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION NUMBER: JP 3-95476
FILING DATE: 19-FEB-1992
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION: NAME: WEGNER, Harold C. REGISTRAION NUMBER: 53-258
REFERENCE/DOCKET NUMBER: 53466/126/AAOI
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAR: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62.2%; Score 520.5;
65.4%; Pred. No. 7.6e
tive 13; Mismatches
                                                                                                                                                                                                                                                                                                                                       53466/126/AAOK
                  RIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117
FILING DATE: 20-DEC-1993
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Patent No. 6114143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               135 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 65.4
Matches 102, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Washington STATE: D.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 112, Application US/08436717

Patent No. 5817790

GENERAL INFORMATION:
APPLICANT: SATO, Koh
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Maxy
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLGY & Lardner
ADDRESSEE: FOLGY & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: Floppy disk COMPUTER: IBM PC compatible OPERAING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: US/08/436 777 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . 6e-46;
20;
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                       CLASSIFICATION: 500

CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992

PRIOR APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 19-FEB-1992

PRIOR APPLICATION NUMBER: JP-EB-1992

PRIOR APPLICATION NUMBER: JP-EB-1992

ATORNEY/AGENT INFORMATION:
NAME: WEGNER: APPR-1991
ATORNEY/AGENT INFORMATION:
NAME: WEGNER: 25,259

REGIGTRATION NUMBER: 25,259

REGIGTRATION NUMBER: 25,259

REGIGTRATION NUMBER: 25,259

REGIGTRATION NUMBER: 25,259

REGIGTRATION NUMBER: 25,259

REGIGTRATION NUMBER: 25,259

REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELESPAN: (202)672-5399

TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62.2%; Score 520.5;
65.4%; Pred. No. 7.6e
tive 13; Mismatches
APPLICATION NUMBER: US/08/137,117D
FILING DATE: 20-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 904136
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111 AVYYCARGGN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 65.4
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , MOLECULE TYPE: protein US-08-137-117D-112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Washington
STATE: D.C.
COUNTRY: USA
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TOPOLOGY: linear
MOLECULE TYPE: polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 6 Becker Fa
CITY: Roseland
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07068
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                                                                                                                                                                                                                               RESULT 11
US-08-477-877B-94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 YIWHWVRQAPQQGLEWIGGINPNNGDISYIQKFKGKAIMTVDISINIAYMELSSLRSEDT 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MDWTWRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: Amino acid OTHER INFORMATION: sequence of H chain V region version r of OTHER INFORMATION: humanized anti-HMI,24 antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/09355925

Patent No. 6503510

GRNERAL INFORMATION:
APPLICANT: KOISHIMMEA, YASUO
APPLICANT: YOSHIMURA, YASUSHI
ITILE OF INVENTION: THERAPEUTIC AGENT FOR LYMPHATIC TUMORS
FILE REPERBENCE: 053466/0555
CURRENT APPLICATION NUMBER: US/09/355,925
CURRENT APPLICATION NUMBER: PCT/JP98/00568
PRIOR PLING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: JP 9-41410
PRIOR FILING DATE: 1997-02-12
PRIOR APPLICATION NUMBER: JP 9-41410
SPRIOR SEQ ID NOS: 8
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 61.8%; Score 517.5; DB 4; Length 139; Best Local Similarity 66.0%; Pred. No. 1.6e-45; Matches 103; Conservative 11; Mismatches 25; Indels 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 137;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 AMYYCARADNYFDIVTGYTSHYFDYWGRGTLVTVSS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111 AVYYCA------TPYYAYAIDSWGQGTLVTVSS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 517.5; DB 3; Pred. No. 1.6e-45; 15; Mismatches 22
APPLICATION NUMBER: US/08/513,968
FILING DATE: 11-SEP-1995
CLASSIFTCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 78913/1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGET L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: 25,618
TELEPHONE: 202-628-5197
TELEPHONE: 202-628-5197
TELEPAX: 202-737-3528
                                                                                                                                                                                                                                                TELEFAX: 202-7-2
TELEFAX: 248633
INFORMATION FOR SEQ. ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 137 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 64.1%;
Matches 100; Conservative 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                           / MOLECULE TYPE: protein US-08-513-968-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              139
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80 INPNSGATDYAHKEQGRVTMSRDTSISTAYMELSRLTSDDTAMYYCARADNYFDIVTGYT 139
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61.6%; Score 516; DB 2; Length 123;
Best Local Similarity 74.5%; Pred. No. 2e-45;
Matches 102; Conservative 8; Mismatches 13; Indels 1
                                                                                                                                                                                                                          TITLE OF INVENTION: LO-CT2A Antibody and Uses
TITLE OF INVENTION: Thereof for Inhibiting
TITLE OF INVENTION: T-C211 Activation and
TITLE OF INVENTION: T-C211 Activation and
TITLE OF INVENTION: Proliferation
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
ADDRESSEE: Cacchi, Stewart & Olstein
STREET: Roseland
CITY: Roseland
STATE: New Jersev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Human Amu 5-3 heavy chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: MS-DUS
SOFTWARE:
Worderfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,969B
FILING DATE: 07-47W-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/407,009
FILING DATE: 29-WAR-1995
APPLICATION NUMBER: 08/119,032
FILING DATE: 06-WAR-1993
APPLICATION NUMBER: 08/027,008
FILING DATE: 06-WAR-1993
ATOMNEN DATE: 05-WAR-1993
ATOMNEN DATE: 01-WAR-1993
ATOMNES: 24,025
CHARACTORNINABRE: 24,025
                                      Sequence 94, Application US/08477989B
Patent No. 5951983
GENERAL INFORMATION:
APPLICANT: Bazin, Herv
APPLICANT: Latinne, Dominique
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: 3.5 inch diskette COMPUTER: IBM PS/2 OPERATING SYSTEM: MS-DOS ACREMANTE
                                                                                                               Bazin, Herv
Latinne, Dominique
Kaplan, Ruth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                140 SHYFDYWGRGTLVTVSS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 123 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                    Kieber-Emmons,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U.S.A.
ZIF: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New Jersey
: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             region.
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NAME/KEY:
US-08-477-989B-94
                                                                                                                                                                      APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
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                                                                                                                                        US-08-472-281A-94
US-08-472-281A-94
Sequence 94, Application US/08472281A
Sequence 95, Application US/08472281A
Sequence 94, Application
Sequence 94, Application
Sequence 94, Application
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 96
CORRESSEDERS: 96
CORRESSEDERS: Garella, Byrne, Bain, Gilfillan,
ADDRESSEDE: Cecchi, Stewart & Olstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80 INPNSGATDYAHKFQGRVTMSRDTSISTAYMELSRLTSDDTAMYYCARADNYFDIVTGYT 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51 INPNSGGTNYAQKFQGRVTWTRDTSISTAYMELSRLRSDDTAVYYCARGRTEYIVV---- 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTG------YYMHWVRQAPQQLEWMGR S0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 QVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTAYSVHWVRQAPGQGLEWMGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13; Indels 14; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human Amu 5-3 heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                   ALDIALOSADER: CECCOII, STEWART & UISTEIL STREET: 6 BECKET FAIM Road CITY: Roseland STREET: New Jersey COUNTRY: New Jersey COUNTRY: U.S.A.

ZIP: 07068
ZIP: 07068
COMPUTER: READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette COMPUTER: IBM PS/2
COMPUTER: APADALE FORM:
MEDIUM TYPE: 3.5 inch diskette COMPUTER: IBM PS/2
COMPUTER: JEM PS/2
COMPUTER: JEM PS/2
COMPUTER: WORTHER: WS-DOS SOFTWARE: WORTHER: WS-DOS SOFTWARE: WORTHER: US/08/472,281A FILING DATE: CO-JUN-1995
CLASSIFICATION NUMBER: 08/407,009
FILING DATE: 29-MAR-1995
APPLICATION NUMBER: 08/119,032
APPLICATION NUMBER: 08/27,008
FILING DATE: 09-SEP-1993
APPLICATION NUMBER: 08/27,008
FILING DATE: 09-MAR-1993
APPLICATION NUMBER: 08/27,008
FILING DATE: OP-MAR-1993
APPLICATION NUMBER: 08/27,008
FILING DATE: OP-MAR-1993
APPLICATION NUMBER: 08/27,008
FILING DATE: OP-MAR-1993
APPLICATION NUMBER: 08/27,008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Olstein, Elliot M.
REGISTATION NUMBER: 24,025
REFERENCE, DOCKET NUMBER: 617
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      140 SHYFDYWGRGTLVTVSS 156
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107 AEGFDYWGQGTLVTVSS 123
140 SHYFDYWGRGTLVTVSS 156
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MOLECULE TYPE: polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 123 amin Typp
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TYPE: amino acid
STRANDEDNESS:
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US-08-472-281A-94
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107 AEGFDYWGQGTLVTVSS 123

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61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTSISTAYMELSRLTSDDT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                               APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: SATO, Koh
APPLICANT: SATO, Koh
APPLICANT: JONES, Steven
APPLICANT: SALDANHA, Jose
APPLICANT: SALDANHA, JOSE
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPEDIBENCE FOLSK Lardner
ADDRESSE: FOLSK Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PACENTE: PC_DOS/NS-DOS SOFTWARE: PACENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/436,717 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AMYYCARADNYFDIVTGYTSHYFDYWGRGTLVTVSS 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
FILING DATE: 24-APR-1992
APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 3.1e
; Mismatches
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PRICATION NUMBER:

FILING DATE: 19-FEB-1992

PRICATION DELGATION DELGA-
APPLICATION DELGA-
FILING DATE: 25-APR-1991

ATORNEY/AGENT INFORMATION:
NAMES WEGNER, Harold C.
RECASTRATION NUMBER: 25,258

REFERENCE/DOCKET NUMBER: 53466/12

TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: (202)672-5309
                    Sequence 102, Application US/08436717; Patent No. 5817790; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Washington
STATE: D.C.
COUNTR: US.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-D
SOFTWARE: PatentIn Release #1
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amino acid
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Best Local Similarity 64.1
Matches 100; Conservative
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TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acid
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US-08-436-717-102
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Best Local Similarity 64.1<sup>5</sup>
Matches 100; Conservative
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                       RESULT 14
US-08-137-117D-102
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Search completed: April 5, 2004, 13:44:09 Job time: 14.9898 secs

us-10-044-569b-6.rai

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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
               Copyright
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- protein search, using sw model OM protein April Run on:

5, 2004, 13:25:01; Search time 11.6142 Seconds (without alignments) 1184.358 Million cell updates/sec

US-10-044-569B-8 738 1 METPAÇLIFILLIMLPDITG.....TKVEIKRIVAAPSVFIFPPS 143 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Searched:

283366 Total number of hits satisfying chosen parameters: 283366 segs, 96191526 residues

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	карра	Kappa	kappa	kappa	i-Sm a	Kappa	light	kappa	kappa	kappa	kappa	kappa	kappa	Sappa	kappa	kappa	kappa	kappa	kappa	kappa	kappa	kappa	kappa	cappa	kappa	kappa	cappa	kappa	карра
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SUMMARIES		20631	PL0106	K3HUHA	кзнині	532	9690	10	643	325	274	637	346	0360	594	327	594	S20633	521	U41	380	0363	3746	627	0379	375	0344	0345	701	4
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de	Query										•	77.3			•			74.3							71.4					
	Score	625.5	619	608.5	598.5	596.5	590.5	585.5	585.5	576	572.5	70.	569	566.5	o	63.		48	m	53		33	32.	m	\sim	S	N	N	52	
	Result No.		7	m	4	w	φ	7	മ	σı	10	11	12	13	14	15	16	17	18	13	20	21	22	23	24	25	26	27	28	29

kappa chain		kappa	kappa chain	kappa chain	kappa chain	kappa	kappa chain	kappa chain	kappa chain	kappa chain	kappa chain	kappa chain	kappa chain	kappa chain	kappa chain
840343	A30608	S40328	K3HUVG	JE0244	B30601	кзничн	S41817	C30601	G30607	E30607	840359	D30601	H44151	H30601	G30601
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128	109	131	115	215	109	116	116	109	109	110	111	109	108	109	109
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ALIGNMENTS

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Ig Kappa chain - human

(g. Kappa chain - human

(g. Species: Homo sapiens (man)

(g. Species: Homo sapiens (man)

(g. Species: Homo sapiens

(g. Mccession: S20631

R. Lee, S. K.; Bridges, L.S.; Koopman, W.J.; Schroeder, H.W.

R. Lee, S. K.; Bridges, L.S.; Koopman, W.J.; Schroeder, H.W.

A. Reference number: S20631

A.; Seetence number: S20631

A.; Status: preliminary

A.; Molecule type: mRNA

A.; Residues: 1-145 < LEE>

A.; Cross-references: EMBL. 211903; NID: g331156; PIDN: CAA77955.1; PID: g331157

C; Superfamily: immunoglobulin V region; immunoglobulin homology

C; Keywords: heterotetramer; immunoglobulin

F; 36-111/Domain: immunoglobulin homology < INM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 PGQAPRLLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPBDFAVYYCQQYGTSALLTF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 PGQAPSLVIYGVSIRATGIPDRFSGSGSETDFTLTISRLEFEDFAVYCHQYGYTP-LTF 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 METPAQLLFLILLWLPETTGEIVLTQSPGTLSLSPGERATLSCRASQKIKONYLAWYQQK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
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84.8%; Score 625.5; DB 2

Best Local Similarity 86.0%; Pred. No. 1.3e-44;

Matches 123; Conservative 5; Mismatches 14
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RESULT 2 PL0106

ig kappa chain precursor V-J-C region (LS1) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C;Accession: PLO106
R;Silberstein, L.E.; Litwin, S.; Carmack, C.E.
B;Silberstein, L.E.; Litwin, S.; Carmack, C.E.
A;Tille: Relationship of variable region genes expressed by a human B cell lymphoma sec
A;Reference number: PLO106; MUID:89235583; PMID:2541221
A;Accession: PLO106.

A;Molecule type: mRNA
A;Residues: 1-144 <SIL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-115/Domain: V region <VRE>

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A; Gener. GDB:136266
A; Cross-references: GDB:136266
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A; Cross-reference: Carchas of two identical light (ka hain disulfide bonds: In some cases, such as IgA and IgW, the subunits associate into l C; Complex: Automatical bonds: In some cases, such as IgA and IgW, the subunits associate into l C; Superfamily: immunoglobulin V region; Immunoglobulin homology
C; Keywords: automatical genence #status preddicted <SIGs-F:1120/Product: Ig kappa chain V-III region (Hic) #status preddicted <MAT>F:21-117/Region: V segment
F:35-111/Domain: immunoglobulin homology <IMM>F:35-111/Domain: immunoglobulin homology <IMM>F:35-111/Domain: complementarity-determining 2
F:10-117/Region: complementarity-determining 3
F:10-117/Region: complementarity-determining 3
F:110-117/Region: J segment (JKL)
F:310-117/Region: J segment (JKL)
F:310-117/Region: J segment (JKL)
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                                                                                                                                                                                                                                                                           the surface immunoglobulin M autoantibodies expressed
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                                                                                     C,Accession: PL0021
R;Kipps, T.J.; Tomhave, E.; Chen, P.P.; Carson, D.A.
Lspps, T.J.; Tomhave, E.; Chen, P.P.; Carson, D.A.
A;Title: Autoantibody-associated kappa light chain variable region gene expressed
A;Reference number: PL0021; MUID:88171307; PMID:3127527
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                                              C;Species: Homo sapiens (man)
C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 PGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPXDFAVYVCQQYGSSP-WTF
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Pred. No. 2.8e-42;
4; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 598.5; DB 1;
Pred. No. 1.9e-42;
3; Mismatches 7;
                      Ig kappa chain precursor V-III region (Hic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81.1%;
ilarity 91.5%;
Conservative 3
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90.8%;
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C, Comment: The protein is one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 90.8
Matches 118; Conservative
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Best Local Similarity
Matches 119; Conserv
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A;Residues: 1-129 <MAH>
                                                                                                                                                                                                                                 A; Molecule type: mRNA
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AyItle: Autoantibody-associated kappa light chain variable region gene expressed in chu
A;Reference number: PL0021; MUID:88171307; PMID:3127527
A;Accession: PL0022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-129 <KIP>
C;Comment: The protein is one of the surface immunoglobulin M autoantibodies expressed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig kappa chain precursor V-III region (Hah) - human
C.Species: Homo sapiens (man)
C.Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 21-Jan-2000
C;Accession: PL0022
                                                                                                                                                                                                                                                         1 METPAQLIFILILIMIPDITGEIVITQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQX
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Pred. No. 2.9e-43;
2; Mismatches 6
                                                                                                                                                          4.46-44;
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R; Kipps, T.J.; Tomhave, E.; Chen, P.P.; Carson, D.A.
                                                                                                                                 Query Match
83.9%; Ścore 619; DB
Best Local Similarity 88.1%; Pred. No. 4.4e-
Matches 126; Conservative 5; Mismatches
F;44-54/Region: complementarity-determining 1
F;70-76/Region: complementarity-determining 2
F;109-115/Region: complementarity-determining 3
F;1108-115/Domain: J region (ARG)
F;128-144/Domain: C region (fragment) <CRE>
                                                                                                                                                                                                                                                                                                                                                                                                                      GGGTKVEIKRTVAAPSVFIFPPS 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGGTKVEIKRTVAAPSVFIFPPS 141
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Best Local Similarity 93.1
Matches 121; Conservative
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A; Residues: 1-129 < KIP>
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PGGAPRILIYGASSRATDIPHRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGTSALLTF 120
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C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                               C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
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A;Cross-references: EMBL:X72435; NID:g441338; PIDN:CAA51103.1; PID:g441339
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: hereroretramer; immunoglobulin
F;35-110/Domain: immunoglobulin homology <IMM>
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                                      61 PGQAPKLLIYGASSRATGIPDRFSGSGSGTDFTLTISKLEPEDFAVYXCQQYGSSP-FPF
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R;Xlein, R.; Jaenichen, R.; Zachau, H.G.
Bur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: $40312; MUID:94080891; PMID:8258341
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Pred. No. 2.3e-41;
6; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78.0%; Score 576; DB 2; L Llarity 84.5%; Pred. No. 1.4e-40; Conservative 11; Mismatches 9;
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A,Scatus: preliminary: translation not shown
A,Molecule type: mRNA
A,Residues: 1-129 <KLE>
                                                                                                                                                                                                                                                                                                                                         kappa chain V region - human (fragment)
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Best Local Similarity 88.5%;
Matches 115; Conservative
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GOGTRLEIKR 129
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Best Local Similarity
Matches 109; Conserv
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A;Molecule type: mRNA
A;Residues: 1-134 <BEN>
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C;Date: OrMay-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: 846369
R;Bensimon, C.; Chastagner, P.; Zouali, M.
R;Bensimon, C.; Chastagner, P.; Zouali, M.
R;Bensimon, C.; Hogst agner, P.; Zouali, M.
A;Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene really. R;Reference number: 846369; MUID:94313975; PMID:8039491
                                                                                                                                                                                                                                                                                                                                                                                   Ig kappa chain V region - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: S20636
R;Lee, S.K.; Bridges, L.S.; Koopman, W.J.; Schroeder, H.W.
submitted to the EMBL Data Library, April 1992
A;Reference number: S20631
A;Accession: S20636
A;Accession: S20636
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                                                                                                    61 PGQAPKLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP-QTF 119
                                                             PGQAPRLLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSALLTF 120
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      METPAQLLFLLLLWLPDTTGEIVLTQSPGTLSLSPGERATLSCRASQSFSSSYLAWYQQK 60
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A;Status: preliminary
A;Molecule type: manny
A;Residues: 1-129 **ABEN>
A;Cross-references: EMBL:227170
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;36-111/Domain: immunoglobulin homology <IMM>
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88.5%; Pred. No. 2.3e-41;
ive 6; Mismatches 8;
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Pred. No. 8.7e-42;
1; Mismatches 9;
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Best Local Similarity 91.5%;
Matches 118; Conservative
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Best Local Similarity
Matches 115; Conserv
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C.Species: Homo sapiens (man)
C.Daces G.Amar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C.Dacession: S40360
R.A.Stein, R.; Jaenichen, R.; Zachau, H.G.
Bur. J. Immunol. 23, 3248-3271, 1993
Bur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
                                                                                                                                                                                                                                                                                                                                                                                                                                        Species: Homo sapiens (man)
Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
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                                                                    61 PGQAPRLLIYGVSSRATGIPDRFSGSASGTDFTLTISRLEPEDFAVYCQHYGGSPRBYT
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C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-200
C;Accession: $40346
C;Accession: $40346
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation. A;Reference number: $40312; MUID:94080891; PMID:8258341
A;Accession: $40346
A;Status: preliminary; translation not shown
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Pred. No. 5.2e-40;
9; Mismatches 12;
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Pred. No. 8.3e-40;
4; Mismatches 12
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                                                                                                                                                                                                                                                                                                                                                                                                               Ig kappa chain V-J-C region - human
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86.9%;
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Best Local Similarity 84.0%;
Matches 110; Conservative
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Best Local Similarity 86.9
Matches 113; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 1-131 < KLE>
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C; Species: Homo sapiens (man)
C; Date: 31-Dec-1989 #sequence_revision 30-Sep-1991 #text_change 21-Jan-2000
C; Date: 31-Dec-1989 #sequence_revision 30-Sep-1991 #text_change 21-Jan-2000
C; Ascession: A32274
R; Newkirk, M.M.; Gram, H.; Heinrich, G.F.; Oestberg, L.; Capra, J.D.; Wasserman, R.L.
A; Cin. Invest. 81, 1511-1518, 1988
A; Title: Complete protein sequences of the variable regions of the cloned heavy and ligh actors of the Wa idiotypic family.
A; Reference number: A92767; MUID:88213701; PMID:2452836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,Residues: 1-130 - CLEE> . A,
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A Molecule type: DNA
A Residues: 1-129 VEEN
A Molecule type: DNA
A Residues: 1-129 VEEN
A Molecule type: DNA
A Residues: 1-129 VEEN
A Mole: the authors translated the codon GAT for residue 17 as Ala
A Note: the authors translated from the differentiated gene
C Suberfamily: immunoglobulin V region; immunoglobulin homology
C Keywords: heterotetramer; immunoglobulin
Fil-20/Domain: signal sequence #status predicted <SIG>F:21-129/Product: Ig kappa chain V-III region EVI-15 #status predicted <KV3>F:36-111/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig kappa chain V region - human
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C;Accession: S20637; S20632
R;Lee, S.K.; Bridges, L.S.; Koopman, W.J.; Schroeder, H.W.
submitted to the EMBL Data Library, April 1992
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Pred. No. 3.9e-40;
2; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11;
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89.2%; Pred. No. 2.6e-40;
tive 2; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                             kappa chain precursor V-III region (EVI-15)
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Conservative
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Best Local Similarity 89.2
Matches 116; Conservative
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                                                                                                         122 GGTKVEIKR 130
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A, Accession: S20637
A, Status: preliminary
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Best Local S:
Matches 114
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A, Status: not compared with conceptual translation
A, Status: not compared with conceptual translation
A, Status: not compared with conceptual translation
A, Molecule type: DNA
A, Note: this sequence was translated from an aberrantly rearranged kappa gene from lambo
G, Genetics:
A, Map position: 2
A, Introns: 17/1
C, Superfamily: immunoglobulin V region; immunoglobulin homology
C, Superfamily: immunoglobulin predicted <SIG>
F, 120/Domain: signal sequence #status predicted <SIG>
F, 121/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                        Ig Kappa chain precursor V-III (Nalm-6) - human C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 19-NOv-1988 #sequence_revision 19-Nov-1988 #text_change 21-Jan-2000
C;Accession: B27594
R;Graninger, W.B.; Goldman, P.L.; Morton, C.C.; O'Brien, S.J.; Korsmeyer, S.J.
T;Graninger, W.B.; Goldman, P.L.; Morton, C.C.; O'Brien, G.J.; Korsmeyer, S.J.
A;Title: The kappa-deleting element. Germline and rearranged, duplicated and dispersed A;Reference number: A92779; MUID:88154739; PMID:3126251
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PGQAPRLLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSALLTF 120
                             61 PGQAPRLLIYDASNRATGIPDRFSGSGSGTDFTLTISRLEPQDFAVYYCQHYGRSPPLTF 120
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Cispecies: Homo sapiens (man)
Cidate: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
Cidatession: 540327
Eur. J. Immunol. 23, 3248-3271, 1993
Arritle: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40327
A;Status: preliminary; translation not shown
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A, Cross-references: EMBL:X72437; NID:g441342; PIDN:CAA51105.1; PID:g441343
C, Superfamily: immunoglobulin V region; immunoglobulin homology
C, Keywords: heterotetramer; immunoglobulin
F;33-108/Domain: immunoglobulin homology <IMM>
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Pred. No. 1.4e-39;
6; Mismatches 5;
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Best Local Similarity 90.2%;
Matches 110; Conservative
                                                                                                                                                          121 GGGTKVEIKR 130
                                                                                                                    GGGTKVEIKR 130
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61
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Db 61 APRLLIYGASSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVFYCQQYGSSP-ITFGQG 119
Oy 124 TK 125
Db 120 TR 121
Search completed: April 5, 2004, 13:43:03
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61 PGQAPRLLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSALLTF 120
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SEQUENCE FROM N.A.
MEDLINE-88171307; PubMed=3127527;
Kipps T.J., Tonhave E., Chen P.P., Carson D.A.;
Kipps T.J., Tonhave E., Chen P.P., Carson D.A.;
Kipps T.J., Tonhave E., Chen P.P., Carson D.A.;
Mutcantibody-associated kappa light chain variable region gene expressed in chronic lymphocytic leukemia with little or no somatic mutation. Implications for etiology and immunotherapy.";
J. Exp. Med. 167:840-852(1988).
-!- DIERASE: The protein is one of the surface immunoglobulin M autoantibodies expressed in patients with chronic lymphocytic
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
MOSI_TaxID=9606,
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FRANEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRANEWOKK-2.
COMPLEMENTARITY-DETERMINING-2.
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COMPLEMENTARITY-DETERMINING-3.
JK1 SEGMENT.
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01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
18 Kappa chain V-III region HAH precursor.
Homo sapiens (Human)
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                                                                                                                                                                                                                               ALIGNMENTS
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HSSP; P80362; 1WTL.
GO; GO:000576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:000555; P:immune response; NAS.
InterPro; IPRO0710; Ig-1ike.
InterPro; IPRO0310; Ig-1ike.
Pfam; PF00047; ig; 1.
SWART; SW00406; iGv; 1.
INTERPOSE INTERPOSE IGV; 1.
IMMUNOGlobulin V region; Signal.
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KV1L_HUMAN
KV2LE_HUMAN
KV3L_MOUSE
KV3N_MOUSE
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1 METPAQLLFLLLLMLPDTTG.....TKVBIKRTVAAPSVFIFPPS 143
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Copyright (c) 1993 - 2004 Compugen Ltd
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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FRAMENOKR-1.
COMPLEMENDARTY-DETERMINING-1.
FRAMEWORK-2.
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MEDLINE-86041852; PubMed=2997711;
Klobeck H.G., Meindl A., Combriato G., Solomon A., Zachau H.G.;
"Human immunoglobulin kappa light chain genes of subgroups II and
                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Pred. No. 9e-45;
3; Mismatches 14; Indels
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FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
JKI SEGMENT.
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                                                  P063II.
P063II.
01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1G Kappa chain V-III region IARC/BL41 precursor.
Homo saplens (Human).
                             128 AA.
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PIR; A01899; K3HU41.
HSSP; P01607; IREI.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; IG-like.
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P. SEQUENCE FROM N.A.

MEDLINE=88171307; PubMed=3127527;

A. Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;

RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;

RT "Autoantibody-associated kappa light chain variable region gene

RT "Autoantibody-associated kappa light chain variable region gene

RT "Autoantibody-associated kappa light chain little or no somatic

RT "Mutatton. Implications for eliology and immunotherapy.";

RL J. Exp. Med. 167:840-852 (1988).

C. -I. DISEASE: The protein is one of the surface immunoglobulin M

CC -I. DISEASE: The protein is one of the surface immunoglobulin M

autoantibodies expressed in patients with chronic lymphocytic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Pred. No. 6.9e-51;
3; Mismatches 7; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KAPPA CHAIN V-III REGION HIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IG KAPPA CHAIN V-III REGION HIC
FRAMENORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMENORK-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPLEMENTARITY-DETERMINING-2. FRAMEWORK-3. COMPLEMENTARITY-DETERMINING-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14070 MW; 7395528EA2BB74D6 CRC64;
                                                                                                                                                                                                                                                                                                     10.1-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
HS-UUL-1999 (Rel. 38, Last annotation update)
HOMO Sapiens (Human).
                                                                                                                                                                                                                                                                                      129 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; PLO021; K3HUHI.
HSSP; PR0362; IWTL.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfan, PF00047; ig; 1.
SMART, SM00406; IGv; 1.
PROSITE, PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81.1%;
ilarity 91.5%;
Conservative
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                                                                                      GGGTKVEIKR 130
                                                                                                                                         GOGTKVEIKR 129
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129 AA;
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Best Local Similarity
Matches 119; Conserv
                                                                                                                                                                                                                                                                                      HUMAN
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NON TER
SEQUENCE
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                                                                                   121
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DOMAIN
DOMAIN
DOMAIN
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KV3M HUMAN
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61 PGQAPRILITYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDPAVYYCQQYGTSALLTF 120
                                                                                  9
                    1 METPAQLIFILIMILPDITGEIVITQSPGTLSLSPGESATLSCRASQSV-SSNLAWYQQK 59
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KV3H HUMAN
ID KV3H HUMAN
AC P04207;
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RESULT 3

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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 METPAQLIFILLIMIPDITIGEIVITQFPGTISISPGERATISCRASQSVASAYLAWYQQK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 PGQAPRLLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYYCQQ 111
                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=85087932; PubMed=6440122;
Pech M., Zachau H.G.;
"Immunoglobulin genes of different subgroups are interdigitated within the VK locus.",
Nucleic Acids Res. 12:9229-9236(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68.6%; Score 506.5; DB 1; Length 115; 91.0%; Pred. No. 4.4e-42; rive 2; Mismatches 7; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IG KAPPA CHAIN V-III REGION VG.
PRAMEMONK-1.
COMPLEMENTARITY-DETERMINING-1.
PRAMEWORK-2.
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COMPLEMENTARITY-DETERMINING-3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Hel. 38, Last annotation update)
Homo sapiens (Human).
chain V-III region VG precursor (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP, P80352; IWTL.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:000382; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X01668; -; NOT ANNOTATED CDS. PIR; A01900; K3HUVG.
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MEDLINE=85087932; PubMed=6440122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM0406; ĪĠv; 1.
PROSITE; PS50835; IG LIKE; 1.
Emmunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  larity 91.0%;
Conservative
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  Ig kappa chain V-III
Homo sapiens (Human)
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es 101, Conserv
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                                                                                       NCBI_TaxID=9606;
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SMART; SM0040
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P04434;
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NON TER
SEQUENCE
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KV3J HUMAN
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Matches
    SOURCE THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DESCRIPTION OF THE TEST TO DE
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                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 PGOPPRLLIYGASTRATGIPARFSGSGSGTEFTLTISKLOSEDFAVYYCOOYNNWPPWTF 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MEAPAQLIFILILIMIPDTTGEIVMTQSPATLSVSPGERATLSCRASGSV-SNNLAWYQQK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 METPAQLIFILLILWIPDTTGEIVLTQFPGTLSLSPGERATLSCRASQSVASAYLAWYQQK
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                                                                                                                                                                                                                     MEDLINE=86177570; PubMed=3083417;
Jirik F.R., Sorge J., Fong S., Heitzmann J.G., Curd J.G., Chen P.P.,
Goldfien R., Carson D.A.;
"Cloning and sequence determination of a human rheumatoid factor
                                                                                          Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
20-MAR-1987 (Rel. 04, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-III region CLL precursor (Rheumatoid factor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72.0%; Score 531.5; DB 1; Length 129; ilarity 82.3%; Pred. No. 2e-44; Conservative 6; Mismatches 16; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IG KAPPA CHAIN V-III REGION CLL. FRANEWORK-1. COMPLEABMENTARITY-DETERMINING-1. FRANEWORK-2. COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
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~hes 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14275 MW; SC13B411BE60CC14 CRC64;
                                                                                                                                                                                                                                                                                                                  light-chain gene.";
Proc. Natl. Acad. Sci. U.S.A. 83:2195-2199(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
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GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006555; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
Ffam; PF004047; 1g; 1.
PRART; EN00406; IGv; 1.
PROSTIE; PS50835; IG_IKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M12740; AAA58992.1; -. HSSP; P80362; 1WTL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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GOGTRVEIKR 129
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129
129 AA;
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Best Local Similarity
Matches 107; Conserv
                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                            NCBI_TaxID=9606;
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13-AUG-1987
15-JUL-1999
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ID KV3I HUMAN
AC P04433;
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SEQUENCE
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DOMAIN
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SOT THE PRESENCE OF THE PRESEN

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Diochemistry 20:5816-5822(1981).

Biochemistry 20:5816-5822(1981).

-1- MISCELLANBOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN ACTIVITY.

REPLANDED TO THE CONTROL OF THE CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN ACTIVITY.

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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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Pred. No. 1.8e-40;
1; Mismatches 9; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 109;
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                                                                                                                                                                                                                                                                                                                                                                                                                   109 AA; 11775 MW; 7689C3ECD646FFB4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66.3%; Score 489.5; DB 1;
88.2%; Pred. No. 1.8e-40;
tive 6; Mismatches 6;
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1996 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
11g kappa chain V-III region WOL.
Homo sapiens (Human).
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               GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; IQ-like.
InterPro; IPR003596; IQ-v.
Pfam; PF00047; ig; 1.
SMART; SMO0406; IGv; 1.
Immunoglobulin V region.
DISULEID
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les 97; Conserv
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                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Biochemistry 20:5816-5822(1981).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA-GLOBULIN ACTIVITY.
PIR; A01892; K3HUSI.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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       Pech M., Zachau H.G.;
"Immunoglobulin genes of different subgroups are interdigitated
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FRAMEWORK-3.
COMPLEMBNTARITY-DETERMINING-3.
BY SIMILARITY.
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Pred. No. 9.7e-42;
5; Mismatches 9; Indels
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FRAMENOKK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
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116 AA; 12757 MW; 51CD55BA53B21929 CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
Homo sapiens (Human)
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GO; GO:0005576; C:extracellular; NAS.

GO; GO:0003823; F:antigen binding; NAS.

InterPro; IPR007110; Ig-like.

InterPro; IPR00556; Ig_v.
                                                                        within the VK locus.";
Nucleic Acids Res. 12:9229-9236(1984)
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Pfam; PF00047; ig; 1.
SMART, SM0406; IGv. 1.
PROSITE; PS56935; IG LIKE; 1.
Immunoglobulin V region; Signal.
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Local Similarity 87.4%;
Les 97; Conservative 5
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P01620;
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SEQUENCE
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FEBS Lett. 2:301-304(1959).
1- MISCELLANEOUS: This is a Bence-Jones protein.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 464.5; DB 1; Length 109;
Pred. No. 4.7e-38;
5; Mismatches 11; Indels 1;
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109 AA; 11830 MW; 9349A5B1D93588B6 CRC64;
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HISSP, BROSG2, 1WTL.
INTERPRO, IPRO07110; IG-like.
INTERPRO, IPRO07110; IG-like.
Pfan, PF00047, 4g, 1.
R SWART; SW00406; IGV; 1.
R PROSITE; PS50835, IG LIKE; 1.
R PROSITE; PS50835, IG LIKE; 1.
W Immunoglobulin, V region; Bence-Jones protein.
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15-JUL-1999 (Rel. 38, Last annotation update)
11g kappa chain V-III region 36.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
reactivity with antipeptide antibodies.";
Mol. Immunol. 23:239-244(1986).
PIR, A01893; K3HUGO.
HSSP, P80362; IWTL.
                                                                                                                           HSSP, F80362; INTI.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
Pfam; PF0047; ig; 1.
SMART; SM00406; IGv; 1.
PROAIT; PS00406; IGv; 1.
Immunoglobulin V region.
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P01619;
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HUMAN
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SEQUENCE
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"The amino acid sequence of the variable regions of the light chains from two idiotypically cross reactive IgM anti-gamma globulins.";
Ann. Immunol. (Paris) 127C:261-271(1976).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN ACTIVITY.
                                                                                                                                                                                                                                                                                                                     "Most kappa immunoglobulin mRNA in human lymphocytes is homologous to a small family of germ-line V genes.";

Nature 307:77-80(1984).

-!- MISCELLANEOUS: THIS GENE WAS ISOLATED FROM THE NG9/9.1 HYBRIDOWA.

PIR, A01894; K3HUNG.

HSSP, 880362; INTL.

GO, GO:0003823; F:antigen binding; NAS.

GO, GO:0005576; C:antigen binding; NAS.

InterPro; IPR007110; Ig-like.

InterPro; IPR003506; Ig-v.

Pfam; PF00047; Ig-like.
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21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
17 kappa chain V-III region POM.
18 kappa chain V-III region POM.
19 kappa chain (Human).
19 kappa chain (Human).
10 kappa chain (Human).
11 kappa chain (Human).
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                         21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1G kappa chain V-III region NG9 precursor (Fragment).
Homo sapiens (Human).
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                                                        100 AA.
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Pfam; PF0047; ig_i.
SWART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Imwunoglobulin V region; Signal; Hybridoma.
SIGNAL
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Bentley D.L.;
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MEDLINE=76276460; PubMed=60899;
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                                                        STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EIVMIQSPVTLSVSPGERATLSCRASQSISNSYLAWYQQRPSGSFRLLIYGASTRATGIP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 EIVLTOFPGTLSLSPGERATLSCRASOSVASAYLAWYQQKPGQAPRLLIYGASSRATDIP 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Gaps
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Klobeck H.G., Bornkamm G.W., Combriato G., Mocikat R., Pohlenz H.D.,
Zachau H.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Subgroup IV of human immunoglobulin K light chains is encoded by
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
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                                                                                                                                                                                                                                                                                                                                                                                          109 AA; 11922 MW; 62821DDC6A8ABA86 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   57.2%; Score 422.5; DB 1; 76.4%; Pred. No. 5.2e-34; iive 11; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
11g kappa chain V-IV region JI precursor.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             133 AA.
                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY.
PIR; A01897; K3HUPM.
HSSP, P80362; JWTL.
GO; GO:0005876; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:000585; F:antigen binding; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
Pfam; PR00047; ig; 1.
PROSITE; SM0406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region.
DISULPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0005576; C:extracellular; NAS. GO; GO:0003823; F:antigen binding; NAS. GO; GO:0006955; P:immune response; NAS: InterPro; IPR007110; Ig-11ke.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single germline gene.";
Nucleic Acids Res. 13:6515-6529(1985).
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SWART; SM00406; iGv; i. -
SMO1TE; PS0835; IG LIKE; i.
Immunoglobulin V region; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                 61 WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYDT- 119
                                                                                                                                                                                                                                                  56 WYQQKPGQAPRLLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTS 115
                                                                                                                                                                                                           1 METPAQLLFLLLLWLPDTTGEIVLTQFPGTLSLSPGERATLSCRASQSVASA----YLA
                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-85014148; PubMed-6091049; Klobeck H.G.; Klobeck H.G., Combriato G., Zachau H.G.; Immunoglobulin genes of the kappa light chain type from two human lymphoid cell lines are closely related."; Nucleic Acids Res. 12:6995-7006(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IG KAPPA CHAIN V-I REGION WALKER. FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
                                                                                                                               56.6%; Score 417.5; DB 1; Length 133; larity 62.2%; Pred. No. 2e-33; Conservative 18; Mismatches 26; Indels 7
 FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
                                        COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
                                                                                     133
14632 MW; 5FB3953066744AF4 CRC64;
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15-AUG-1999 (Rel. 38, Last annoration update)
15 kappa chain V-I region Walker precursor.
Homo sapiens (Human).
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                                                                         BY SIMILARITY
                               FRAMEWORK-3
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30; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:000855; F:immune response; NAS.
InterPro; IPR007110; Ig-like.
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PIR; AOLGB3; KIHUWK.
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Pfam; PF00047; ig; 1.

PROSITE; PS50835; IG LIKE; 1.

Immunoglobulin V region; Signal.

SIGNAL

23 129 IG KF
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62 PGKAPKLLIYAASSLQSGVTSRFSGSGSGTDFTLTISSLQPEDSATYXCQQ-SYSTLITF 120
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                                                                                                                                     9
                                                                                                                                                   3 MRVPAQLIGILILMLRGARCDIQMTQSFSSLSASVGDRVTITCRASQSI-SNYLNWYQQK 61
                                                                                                                                     1 METPAQLLFLLLLWLPDTTGEIVLTQFPGTLSLSPGERATLSCRASQSVASAYLAWYQQK
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                                                                             54.7%; Score 404; DB 1; Length 129; 64.3%; Pred. No. 3.8e-32; ive 15; Mismatches 29; Indels
COMPLEMENTARITY-DETERMINING-3.
                                                    14069 MW; F941FA07D4AFC2F9 CRC64;
              FRAMEWORK-4.
BY SIMILARITY
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83; Conservative
 119
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121 GQGTRLEIK 129
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Q9RIA5 Q91W12 Q91W12 Q8K1F2 Q92OE9 Q9QYF0 Q8V1J0 Q8V1J0 Q911U6 Q9110 Q92D9 Q91178 Q91178 Q91178

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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MEDLINE=98277139; PubMed=9614934;
MU X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9UL78;
01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
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Licus.;
Lin. Immunol. Immunopathol. 87:184-192(1998).

EMEL, AF035036; AAD56272.1; -.

PIR, A30601; A30608.

PIR, B30601; B30601.

PIR, B30601; B30601.

PIR, B30607; B30607.

PIR, C30608; C30608.

PIR, C30609; C30608.

PIR, C30609; P30601.

PIR, D30601; D30601.

PIR, P30607; P30607.

PIR, F30607; P30608.

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PIR, P30608; P30608.

PIR, B30608; P30608.

PIR, H30608; P30609.

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PIR, H30609; P30609.
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1 METPAQLLFLLLMLPDTTG.....TKVEIKRTVAAPSVFIFPPS 143
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Perfect score:
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109 AA.

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            Q72473
ID Q72473
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                                                                                                                                                                                                                               80
                                                                                                                                                                                                                                           1 EIVLTQSPGTLSLFPGERATLSCRASQSVSSSYLAWYQQKPGQAPKLLIYGTSSRATGIP 60
                                                                                                                                                                                                                               EIVLTOFPGTLSLSPGERATLSCRASOSVASAYLAWYQQKPGQAPRLLIYGASSRATDIP
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DRFSGSGSGTDFTLTISRLEPEDCAVYYCQQYGSSP-LTFGGGTKVEIKR 109
                                                                                                                                                                                                                                                                                 81 HRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSALLTFGGGTKVEIKR 130
                                                                                                                                                                        Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                    01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin kappa chain variable region
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                                                                                                                                               5F675C52EC7EE197 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 483.5; DB 4;
Pred. No. 1.1e-41;
5; Mismatches 8;
                                                                                                                                                                      Ouery Match
Best Local Similarity 91.8%; Pred. No. 6.3e-44;
Matches 101; Conservative 3; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998)
EMBL, AF035028; AADS6264.1; -.
PIR, B30607; B30607.
                                                                                                                                                                                                                                                                                                                                                                              109 AA.
                                                                                                                                                                                                                                                                                                                                                                                        Q9UL86;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
01-Crt. 2003 (TrEMBLrel. 25, Last ann
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                                  HSSP, P80362; IWTL.
INTERPRO; IPR007110; Ig-like.
INTERPRO; IFR003596; Ig-v.
Ffam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP, P80362; 1WTL.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PR0STTE; PS5035; IG_LKE; 1.
                                                                                                                                              109 AA; 11646 MW;
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PIR; PH0963; PH0963.
PIR; PH0965; PH0965.
PIR; S34096; S34096.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 PGKAPQLLIYAASTLQSGVPSRFSGSASGTDFTLSISCLQSEDFATYYCQQYYTYP-WTF 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 METPAQLLFLLLLWLPDTTGEIVLTQFPGTLSLSPGERATLSCRASQSVASAYLAWYQQK
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0.1-0CT-2002 (TrEMBLrel. 22, Last sequence update)
0.1-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Hypothetical protein.
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                  Eukaryoca, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC056256; AAH56256.1;
Hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               234 AA; 25674 MW; 1A2C259BAB51BC0F CRC64;
                                                                                Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA sequences.";
1. Acad. Sci. U.S.A. 99:16899-16903(2002)
234 AA
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PRT;
                                                                           01-0CT-2003 (TrEMBLrel. 25, 01-0CT-2003 (TrEMBLrel. 25, 01-0CT-2003 (TrEMBLrel. 25, Hypothetical protein.
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PRELIMINARY;
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and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                           [2]
SEQUENCE FROM N.A.
TISSUE-Skeletal muscle;
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TISSUE=Lung;
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Best Local S
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Q8TCD0
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TISSUESKeletal muscle;

XX MEDINELS288257; PubMed=12477932;

XX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

X Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,

X Strausberg R.L., Peingold E.A., Grouse L.H., Schamen C.M., Schuler G.D.,

X Alachul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Blank N.K.,

Alachul S.F., Zeeberg W.B., Buetow K.S.I., Wang J., Heine H.,

Nores T., Max S.I., Mond G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

XN Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Yillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rachard M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Nhiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Rachiguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                             Gaps
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
Eukaryota, Metazoa, Chordata; Craniata, Vertebrata; Euteleostomi;
Mammalia, Eutheria, Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                            2,
                                                                                                                                                                                                                                                                                                                 Length 239;
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                                                                     to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                    F5E20AD3B0552C0A CRC64;
                                                                                                                                                                                                                                                                                                               Query Match 62.4%; Score 460.5; DB 4;
Best Local Similarity 62.6%; Pred. No. 6.8e-39;
Matches 92; Conservative 22; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 LLTFGGGTKVEIKRTVAAPSVFIFPPS 143
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                                                                                                                                                                                             Pfam: PF00047, 19, 2-7.
SMART; SM0407, 19.
SMART; SM0407, 19.
SMART; SM0406, 10.
PROSITE; PS50835; 10_LIKE; 2.
PROSITE; PS00290; 10_MHC; 1.
Hypothetical protein. 26024 MW; FF
                                                    Strausberg R.;
Submitted (JUN-2002) to the EMBI
EMBL; 80030814, 13 -..
PIR; S23638; S23638.
PIR; S34091; S34091.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig-c1.
InterPro; IPR003596; Ig-MC.
                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                     61 PGQAPRLLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSALLTF 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 METPAQLLFLLLLMLPDTTGEIVLTQFPGTLSLSPGERATLSCRASQSVASAYLAWYQQK
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
Strausberg R.;
Strausberg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC022362; AAH22362.1; -.
PTR; S42267; S42267.
PTR; S42268; S42268.
PTR; S42268; S42268.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_WHC.
InterPro; IPR00306; Ig_WHC.
Refervo; IPR00306; Ig_WHC.
Refervo; IPR00306; Ig_WHC.
Refervo; IPR00306; Ig_W.
Pfam; PF00040; IGv; 1.
Refervo; PF00209; IG_MHC; 1.
Refervo; PROSITE; PS00209; IG_MHC; 1.
Refervo; PROSITE; PS00209; IG_MHC; 1.
Refervo; PROSITE; PS00209; IG_MHC; 1.
Refervo; PROSITE; PS00209; IG_MHC; 1.
Refervo; PROSITE; PS00209; IG_MHC; 1.
Refervo; PROSITE; PS00209; IG_MHC; 1.
Refervo; PROSITE; PS00209; IG_MHC; 1.
Refervo; PROSITE; PS00209; IG_MHC; 1.
Refervo; PROSITE; PS00209; IG_MHC; 1.
                                                                                                                                                                               Length 236
                                                                                                                                                                               61.7%; Score 455; DB 4; Length 23, 65.7%; Pred. No. 2.5e-38; arive 16; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28; Indels
Strausberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC005332; AAH05332.1;
Hypothetical protein.
SEQUENCE 236 AA; 25702 MW; 7FBFE4ED23084BC6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-07N-2002 (TrEMBLrel. 21, Created)
01-07N-2002 (TrEMBLrel. 21, Last sequence update)
01-07T-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60.1%; Score 443.5; DB 4;
59.2%; Pred. No. 3.7e-37;
ive 27; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 GGGTKVEIKRTVAAPSVFIFPPS 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 GQGTKLEIKRTVAAPSVFIFPPS 143
                                                                                                                                                                                                               Best Local Similarity 65.7%
Matches 94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87; Conservative
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1 BIVMTQSPATLSVSPGERATLSCWASQSI-SSNLAMYQQKPGQAPRLLIYGASTRATGIP 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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O'1-OCT-2003 (TERMELRE1. 25, Last sequence update)
01-OCT-2003 (TERMELRE1. 25, Last sequence update)
Hypothetical protein.
Menopus laevis (African clawed frog).
Eukaryota, Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                 Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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MEDLINE=22341132; PubMed=12454917;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genetic and genomic tools for Xenopus research: The NIH Xenopus initiative.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Myosin-reactive autoantibodies in rheumatic carditis and normal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin kappa chain variable region
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109 AA; 11761 MW; FB1E43E7C7AFACCC CRC64;
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Local Similarity 79.1%; Pred. No. 7e-37;
Les 87; Conservative 10; Mismatchem 10.
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EMBL; AF035029; AAD56265.1; -.
PIR; D30609; D30609.
                                                                                                                                               109 AA.
PSTFGQGTKLEIKRTVAAPSVFIFPPS 146
                                                                                                                                                                                                           Created)
                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP, P80362, IWTL.
InterPro; IPR007110, IG-like.
InterPro; IPR003596, Ig_v.
Pfam, PF00047; ig, 1.
SMART; SM0406; IGv; 1.
                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-CT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dev. Dyn. 225:384-391(2002)
                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                              (Fragment).
Homo sapiens (Human)
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SEQUENCE FROM N.A.
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                                                                                     RESULT 7
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64 APRILIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSALLTFGGG 123
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01-070-2001 (TrEMBLrel. 17, Last sequence update)
01-077-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Hybothetical protein.
Everyorist (Mouse).
Eukaryota, Metazca; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Musinae; Musinae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 56.6%; Score 418; DB 13; Length 237; Local Similarity 62.9%; Pred. No. 1.5e-34; es 88; Conservative 16; Mismatches 32; Indels
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Strausberg R.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC0020235; AAH02035.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Klein S., Strausberg R.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO54155; AAH54155.1; -.
Hypothetical protein.
SEQUENCE 237 AA; 26300 MW; 47BBDDD2639CB436 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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TRVELKRNDAKPAVFIFKPS 145
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TISSUE=Whole;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI TaxID=10090
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C32248;
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Q99M37
S WAR REPORT OF STANDING SO SERVING SO SERVING SO SERVING SO SERVING SO SERVING SO SERVING SO SERVING SO SERVING SO SERVING SERVING SO SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING
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60 -YLQKPGQSPKILIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQ-STHV 118
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Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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MEDLINE=98277139; PubMed=9614934;
Mu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 56.0%; Score 413; DB 11; Length 238; Best Local Similarity 55.8%; Pred. No. 4.8e-34; Matches 82; Conservative 28; Mismatches 31; Indels 6
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein.
SEQUENCE 238 AA; 26224 MW; 35EC08E3DE5414AD CRC64;
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EMBL; AF035031; AAD56267.1; -.
PIR; B30609; B30609.
PIR; C30609; C30609.
PIR; D30609; D30609.
PIR; S34098; S34098.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 PPTFGGGTKLEIKRADAAPTVSIFPPS 145
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InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro, IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 2.
SMART; SM00406; IGV; 1.
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PROSITE; PSS0835; IG_LIKE; 2.
PROSITE; PS00290; IG_MHC; 1.
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SMART; SM00406; IGv; 1.
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; S26334; S26334.
; S53750; S53750.
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PT0359;
S07455;
S16112;
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PH1034;
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Best Local Similarity 55.8%; Pred. No. 3e-34;
Matches 82; Conservative 28; Mismatches 31; Indels
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Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

R Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

R PIR, A27887, A27887.

R PIR, A33833, A33933.

R PIR, B37887, B37887.

R PIR, B31485, B31485.

R PIR, B31446; B41940.

R PIR, B41446; B41940.

R PIR, C32248, C32248.

R PIR, C32248, C32248.

R PIR, C32349, C34904.

R PIR, D29380, D29380.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      238 AA
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PIR, S07455, S07455.
PIR, S16112, S16112.
PIR, S24500, S24500.
PIR, S24501, S24501.
PIR, S24503, S24503.
PIR, S24504, S24504.
PIR, S24504, S24504.
PIR, S24532, S24532.
PIR, S24533, S24532.
PIR, S24533, S24532.
PIR, S24533, S24532.
PIR, S24536, S24532.
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PROSITE, PS002596, IG_WHC, I.
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A Straubberg R.;
Submitted (UUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC031498; A#131498.1; -.
EMBL; BC031498; A#3333.
R PIR; A3393; A3393.
R PDB; IRN2; 13-MAR-02.
CO; GO:0016491; F:oxidoreductase activity; IEA.
R GO; GO:0018491; F:oxidoreductase activity; IEA.
InterPro; IPR002198; ADH_short.
R InterPro; IPR002109; IG.
IN InterPro; IPR003109; IG.
IN InterPro; IPR003109; IG.
IN InterPro; IPR003597; IG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 PGKSPKTLIYRANRLVDGVPSRFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFP-RTF
                                                                                                                               EIVMTQSPATLSVSPGERATLSCRASQSV-SSNLAWYQQKPGQAPRLLIYCASTRATGIP
                                                                                                                21 EIVLTQFPGTLSLSPGERATLSCRASQSVASAYLAWYQQKPGQAPRLLIYGASSRATDIP
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                                                                                       2; Gaps
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Mus musculus (Mouse).
Mus musculus (Mouse).
Mammalia, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia, Euteria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
1731 TaxID=10090;
                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                         MEDIINE 93383497; PubMed=8372513; Torge D.W., Henmam J.F., Greene A.R., Lee I.D., Edge M.D.; Chorge D.W., Henmam J.F., Greene A.R., Lee I.D., Edge M.D.; Cloning and characterization of 1116(NS19.9 heavy and light chain cDNAs and expression of antibody fragments in Escherichia coll."; Para Immunol. 7:56-62(1993).

EMBL; S65911; AAR28160.11; - SEQUENCE 236 AA; 26454 MW; 2C586EBF5EA10F4C CRC64;
                                                                                                                                                                                 AFFSGSGSGTEFTLTISSLQFEDFAVYYCQHYNNWP-FTFGPGTKVDIKR 108
                                                                                                                                                                  81 HRFSGSGGGDFTLTISRLEPEDFAVYYCQQYGTSALLTFGGGTKVEIKR 130
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                                                              Length 108;
                                                                                       Indels
                                     11834 MW; 9F9C5A92EBA96EEA CRC64;
                                                                                                                                                                                                                                                                              01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Anti-colorectal carcinoma light chain.
                                                            Score 411; DB 4; Le
Pred. No. 2.8e-34;
7; Mismatches 15;
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STRAIN=CZECH II; TISSUE=Breast tumor;
MEDLINE=22388257; PubMed=12477932;
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|GGTKLEIKRADAAPTVSIFPPS 143
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  PS50835; IG_LIKE; 1.
                                                              55.7%;
78.2%;
                                                Query Match
Best Local Similarity 78.4*
Best Local 86; Conservative
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                                                                                                                                                                                                                                                        PRELIMINARY;
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                           108
                         108 AA;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
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             NON TER
NON TER
SEQUENCE
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PROSITE;
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Raussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Schamen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
& Bothero M., Soares M.B., Bonaldo M.F., Carainor D., Hong L.,
& Stapleton M., Soares M.B., Bonaldo M.F., Carainor P.L., Scheetz T.E.,
& Brownstein M.J., Usdin T.B., Tooshiyuki S., Carainor P.D., Mullahy S.J.,
& Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
& Raba S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
& Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
& Richards S., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,
& Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
& Rakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
& Rodriguez A.C., Galmwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
& Rodriguez A.C., Galmwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
& Rodriguez A.C., Galmwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
& Goneration and initial analysis of more than 15,000 full-length human
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Mus musculus (Mouse).

Mus musculus (Mouse).

Mus musculus (Mouse).

Mus musculus (Mouse).

Mus musculus (Mouse).

Mus musculus (Mouse).

Mus Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; M
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54.7%; Score 404; DB 11; Length 2
Best Local Similarity. 56.6%; Pred. No. 4e-33;
Matches 81; Conservative 21; Mismatches 39; Indels
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Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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STRAIN-CZECH II; TISSUE-Breast tumor;
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(TrEMBLrel. 22, Last sequ
(TrEMBLrel. 25, Last anno
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57 YQQKPGQAPRLLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSA 116
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                                                                                                                                                                                                                                           1 METPAQLIFILLIMUPDITGEIVLIQFPGTLSLSPGERATLSCRASQSV----ASAYLAW 56
                                                                                                                                                                                                                                                            2; Gaps
                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                             DB 11; Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 52.7%; Score 389; DB 11; Length 234; l Similarity 55.9%; Pred. No. 1.3e-31; 80; Conservative 21; Mismatches 40; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
REMBL; BC019474; AAH19474.1; -.
REMBL; BC019474; AAH19474.1; -.
RINterPro; IPR007310; Ig-like.
RINterPro; IPR007306; Ig MHC.
RINterPro; IPR007306; Ig WHC.
R Pfam; PF00047; Ig; 2.
R Pfam; PF00047; Ig; 2.
R PROSITE; PS00209; IG MHC; 1.
R PROSITE; PS00209; IG MHC; 1.
R PROSITE; PS00209; IG MHC; 1.
R PROSITE; PS00209; IG MHC; 1.
                                                                                                                                                                             Query Match 52.9%; Score 390.5; DB 11; Length Best Local Similarity 55.1%; Pred. No. 9.7e-32; Matches 81; Conservative 24; Mismatches 37; Indels
InterPro; IPR003596; Ig_v.

Pfam; PP00047; ig; 2.

SMART; SM00407; Ig; 2.

SMART; SM00407; IGc1; 1.

SMART; SM00406; IGv; 1.

PROSITE; PS00061; ADH SHORT; 1.

PROSITE; PS00061; IG_IKE; 2.

PROSITE; PS00290; IG_MHC; 1.

Hypothetical protein.

SEQUENCE 239 AA; 26366 MW; D7BE84398AA341F0 CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        234 AA.
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Best Local Similarity
Matches 80; Conserv
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738
1 METPAQLLFLLLLWLPDTTG.....TKVEIKRTVAAPSVFIFPPS 143
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Aau74299
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                                                                                                           Perfect score:
Sequence:
                                                                                                                                          Scoring table:
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                                                                                                                                                                       Searched:
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                                                                                                   Title:
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Human	0		'n		Human	Aao14066 Light cha	_		Add01357 Human imm	Aar38673 F105Vk-F	Human	Aau33249 Novel hum	Aau14462 Human nov	Aau14463 Human nov	Aau14461 Human nov	Aau14464 Human nov	Aab99378 Human int	Aab75011 Anti-IL8	99397 Human in
Aag	Abg(St dA	Aaw	Aar	Ado	Aao	Abu	Aar	Add	Aar	Aam	Aau	Aau	Aau	Aau	Aau	Aab	Aab.	Aab99
AAG71272	ABG63490	ABJ36930	AAW11155	AAR38672	ADC61062	AA014066	ABU08018 .	AAR41286	ADD01357	AAR38673	AAM24101	AAU33249	AAU14462	AAU14463	AAU14461	AAU14464	AAB99378	AAB75011	AAB99397
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236	236	130	134	129	128	234	234	129	235	129	384	178	384	384	384	384	226	226	226
82.5	82.5	82.3	81.8	81.6	80.4	79.3	79.3	79.1	79.1	78.7	78.4	78.0	78.0	78.0	78.0	78.0	77.9	77.9	77.4
609	609	607.5	604	602.5	593.5	585	585	583.5	583.5	580.5	578.5	575.5	575.5	575.5	575.5	575.5	575	575	571

ALIGNMENTS

RESULT 1

Monoclonal antibody; variable region; heavy chain; light chain; VH; VL; complementarity determining region; CDR; MAb; BO2C11; Conformational belicop; factor VIII; KRXII; von Willebrand factor; hemostasis; intravascular coagulation; arterial thrombosis; arterial restenosis; venous thrombosis; arteriosclerosis. Novel cell lines for producing monoclonal antibodies that bind to a factor involved in hemostasis and coagulation cascade, useful for treating and preventing coagulation disorders. Light chain variable region VL of KRIX1. Location/Qualifiers AAB47061 standard; protein; 143 AA 43. .54 /label= CDR1 69. .75 /label= CDR2 99GB-00016450. Jacquemin MG, Saint-Remy JR; 13-JUL-2000; 2000WO-EP006677. (LEUV-) LEUVEN RES & DEV VZW 109. .118 /label= CDR3 (first entry) WPI; 2001-138333/14. N-PSDB; AAC85454. WO200104269-A1 14-JUL-1999; 14-JUL-1999; Homo sapiens 08-MAY-2001 18-JAN-2001 AAB47061; Key Domain Domain Domain AAB47061

Example 5; Fig 9; 55pp; English

N-PSDB; AAL49257

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This sequence represents the light chain variable region of the monoclonal antibody (RAD), KRIXI. This MAD produced by the cell line of the invention, specifically recognises the wild type factor VIII light chain. KRIXI can be used to inhibit the binding of factor VIII to von Willebrand factor in a dose dependant manner. The new cell line KRIXI, is deposited with the Belgian Coordinated Collections of Micro-organisms, under accession number LMBP 5089CB. KRIXI, or fragments of it, optionally with a thrombolytic agent, are useful for the treatment and/or prevention of hemostasis, coagulation disorder or thrombosic pathologic condition such as intravascular coagulation, arterial thrombosis, arterial restenosis, venous thrombosis or arteriosclerosis, and attenuation of coagulation in a mammal. An effective and safe antithrombotic therapy is provided which reduces the risk of bleeding in mammals, more particularly
                                                                                                                                                                                                                                                                                                                                                                                                           120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, antibody; BO2CII; KRIXI; light chain; heavy chain; inflammation; variable region; factor VIII inhibitor; sepsis; septic shock; thrombus formation; systemic inflammatory response syndrome; CDR; disseminated intravascular coagulation; haemophilia A; immunosuppressive; complementarity determining region; antibacterial; antiinflammatory.
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                                                                                                                                                                                                                                                                                                                                                              METPAQELFILLLMLPDTTGEIVLTQFPGTLSESPGERATLSCRASQSVASAYLAWYQQK
                                                                                                                                                                                                                                                                                                                                           1 METPAQLIFILLIMIPDITGEIVLTQFPGTLSLSPGERATLSCRASQSVASAYLAWYQQK
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                                                                                                                                                                                                                                                                          100.0%; Score 738; DB 4; Length 143; 100.0%; Pred. No. 3e-47; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human KRIX1 light chain variable region.
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/label= CDR1
69. .75
/label= CDR2
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/label= CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                             Local Similarity 100.
nes 143; Conservative
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                                                                                                                                                                                                                                              Sequence 143 AA;
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                                                                                                                                                                                                                   in humans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial; immunostimulant; anti-HIV; hyperproliferative; cancer; viral; bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy; human; light chain; 24-2-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New chimeric or human monoclonal antibody or its antigen-binding portion that specifically binds to and activates human CD40, useful for enhancing an immune response in a human, or treating cancer, HIV, neutropenia or viral infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120
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                                                     Pharmaceutical composition for treating systemic inflammatory response syndrome, sepsis, septic shock and/or thrombus formation in microvasculature in mammals, comprises a partial inhibitor of factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 METPAQLIFLLLIMIPDTTGEIVLTQFPGTLSISPGERATISCRASQSVASAYLAWYQQK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 738; DB 5; Length 143; 100.0%; Pred. No. 3e-47; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGTKVEIKRTVAAPSVFIFPPS 143
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                                                                                                                                                                                                                        Disclosure, Fig 13; 41pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADE28481 standard; protein; 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JAN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100. Matches 143, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gladue RP,
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N-PSDB; ADE28480.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 143 AA;
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The invention relates to a novel chimeric or human monoclonal antibody or its antigen-binding portion that specifically binds to and activates human CD40. The anti-Ord antibody in the invention demonstrates cytostatic, virucide, antibacterial, immunostimulant and anti-HIV activities and may be useful for treating a hyperproliferative disorder such as cancer, viral and bacterial infection or genetic, primary or combined immunodeficiency conditions including neutropenia or HIV in fection. The anti-CD40 antibodies may also be useful for detecting CD40 in a biological sample in vitro or in vivo, as well as during gene therapy procedures. The current sequence is that of the human anti-CD40 antibody full length light chain protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                    118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel antibodies capable of binding cytotoxic T-lymphocyte antigen (CTLA) -4 containing specified heavy and light chain sequences, useful for treating, e.g. immune disorders.
                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                         Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system; hyperimmunity disorder; autoimmune disease; diabetes; graft rejection; proliferative disorder; cancer; immunodeficient disorder.
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                                                                                                                                                                                                                                                                                                                                                          PGQAPRILLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSALLTF
                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Davis CG;
                                                                                                                                                                                                                                                                      7
                                                                                                                                                                                                                                         Length 234;
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                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                        Score 667; DB 7; Le
Pred. No. 8.3e-42;
3; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hanke JH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The kappa chain of immunoglobulin clone 4.1.1.
               Claim 7; SEQ ID NO 88; 177pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                   143
                                                                                                                                                                                                                                                                                                                                                                                                                                     GPGTKVDIKRTVAAPSVFIFPPS 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mueller
                                                                                                                                                                                                                                      90.4%;
Best Local Similarity 92.3%;
Matches 132; Conservative 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-442647/38.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAA46865
                                                                                                                                                                                                               Sequence 234 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-DEC-1999;
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The present sequence represents a kappa chain of an antibody of the invention. The antibody is directed cytotoxic T-lymphocyte antigen (CTLA) -4. Antibodies of the invention are composed of a heavy chain variable region, comprising a modified contiguous sequence from a FR1-FR3 sequence encoded by a human VH3-33 family gene. The modifications are contained in CDR1, CDR2 and/or framework regions. The antibodies may be used to thinbib trula-4 and down-regulate the immune system to treat hyperimmunity disorders (e.g. autoimmune disease, diabetes and graft rejection) and proliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be used to used to up-regulate immune system to up-regulate immune system to up-regulate immunodeficient
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel antibodies capable of binding cytotoxic T-lymphocyte antigen (CTLA) -4 containing specified heavy and light chain sequences, useful for treating, e.g. immune disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system; hyperimmunity disorder; autoimmune disease; diabetes; graft rejection; proliferative disorder; cancer; immunodeficient disorder.
                                                                                                                                                                                                                                                                                                      1 METPAQLIFILLIMIPDTTGEIVLTQSPGTLSLSPGERATLSCRASQSISSSFLAWYQQR
                                                                                                                                                                                                                                                                                    1 METPAQLLFLLLLWLPDTTGEIVLTQFPGTLSLSPGERATLSCRASQSVASAYLAWYQQK
                                                                                                                                                                                                                                                                                                                                                 61 PGQAPRLLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSALLTF
                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Davis CG;
                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                          Length 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neveu MJ, Mueller EE, Hanke JH, Gilman SC,
                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                      90.3%; Score 666.5; DB 3; ilarity 91.6%; Pred. No. 9.1e-42; Conservative 5; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The kappa chain of immunoglobulin clone 4.1.1.

    .20
    /note= "signal peptide"

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                                                                                                                                                                                                                                                                                                                                                                                                              121 GGGIKVEIKRIVAAPSVFIFPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                          GOGTKVEIKRTVAAPSVFIFPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY93729 standard; protein; 235
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                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAA46893.
                                                                                                                                                                                              Sequence 235 AA;
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Corvalan JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JUN-2000
                                                                                                                                                                                                                                                       Matches 131;
                                                                                                                                                                 disorders
                                                                                                                                                                                                                      Query Match
Best Local &
                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                             120
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         The present sequence represents a kappa chain of an antibody of the invention. The antibody is directed cytotoxic T-lymphocyte antipled (CILA) 1. Antibodies of the invention are composed of a heavy chain variable region, comprising a modified contiguous sequence from a FRI-FR3 sequence encoded by a human VH3-33 family gene. The modifications are contained in CDR1, CDR2 and/or framework regions. The antibodies may be used to inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity disorders (e.g. antoimmune disease, diabetes and graft rejection) and proliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be used to up-regulate immune system to up-regulate immunodeficient
                                                                                                                                                                                                                                                                                                                                                                    119
                                                                                                                                                                                                                                                                                                                                      PGQAPRILIYGASSRATDIPHRFSGSGSTDFTLTISRLEPEDFAVYYCQQYGTSALLTF 120
                                                                                                                                                                                                                                                                           1 METPAQLLFLLLLWLPDTTGEIVLTQFPGTLSLSPGERATLSCRASQSVASAYLAWYQQK 60
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                                                                                                                                                                                                                                                                                              61 PGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSP-WTF
                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Use of human anti-cytotoxic T lymphocyte antigen-4 antibody in the preparation of medicament for the treatment of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytotoxic I lymphocyte antigen-4; therapy; CTLA-4 antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Mature anti-CTLA-4 antibody kappa chain"
                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                   Length 235;
                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                   Score 666.5; DB 3;
Pred. No. 9.1e-42;
5; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          anti-CTLA-4 antibody kappa chain.
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/label=_Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                            120 GOGTKVEIKRTVAAPSVFIFPPS 142
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                                                                                                                                                                                                                 Query Match
Best Local Similarity 91.6%;
Matches 131; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-131215/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAD54344.
                                                                                                                                                                                         Sequence 235 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cancer.
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PGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSP-WTF 119
                                                                                                                                                                                                                                                                                                                                 PGQAPRLLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSALLTF 120
The invention relates to the use of human anti-cytotoxic T lymphocyte antigen-4 (anti-CTLA.4) antibody in the preparation of a medicament for the treatment of cancer such as bone cancer, pancreatic cancer, skin cancer, cutaneous or intraocular malignant melanoma, uterine and ovarian cancer, cancer of the anal region, stomach cancer, breast cancer, cancer cancer, and region, stomach cancer, breast cancer, testicular cancer, uterine cancer and carcianoma of the fallopian tubes. The present sequence is human anti-CTLA-4 antibody kappa chain
                                                                                                                                                                                                                                                                                Human; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiallergic; antiulcer; neuroprotective; antithyroid; vasotropic; immunosuppressive; dermatological; antiinflammatory; hepatotropic; activation inducible lymphocyte immunomodulatory molecule; AILIM; monoclonal antibody; allergy; rheumatoid arthritis; diabetes mellitus; multiple sclerosis; autoimmune thyroiditis; psoriasis; hepatitis; allergic contact-type dermatitis; chronic inflammatory dermatosis; systemic lupus erythematosus; autoimmune disorder; inflammation; graft versus host reaction; immune rejection; intestinal immunity; ulcerative colitis; pneumonia; nephritis; vasculitis; pancreatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a novel human antibody (I), preferably a human
                                                                                                                                                                                                                                                          1 METPAQLIFILLIMIPDITGEIVLTOFPGTISISPGERATISCRASQSVASAYLAWYQQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New human monoclonal antibody that binds to activation inducible lymphocyte immunomodulatory molecule, useful for treating rheumatoid arthritis, multiple sclerosis and inflammation.
                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anti-human AILIM monoclonal antibody clone Jmab-138, light chain.
                                                                                                                                                                                                                         1;
                                                                                                                                                                                      Length 235;
                                                                                                                                                                                                                       Indels
                                                                                                                                                                                      Score 666.5; DB 6;
Pred. No. 9.1e-42;
5; Mismatches 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     120 GOGTKVEIKRTVAAPSVFIFPPS 142
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30-MAR-2001; 2001JP-00099508.
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                                                                                                                                                                                    Query Match
Best Local Similarity 91.6%;
Watches 131; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-075313/10.
N-PSDB; AAS99475.
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                                                                                                                                                   Sequence 235 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200187981-A2
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monoclonal antibody which binds to an activation inducible lymphocyte immunomodulatory molecule (AILIM). (i) is useful for modulating signal transduction into a cell mediated by AILIM, for modulating proliferation of AILIM-expressing cells, for modulating production of a cyrokine from AILIM-expressing cells, for inducing antibody-dependent cytotoxicity against AILIM-expressing cells and/or immune cytolysis or apoptosis of AILIM-expressing cells, and/or immune cytolysis or apoptosis of AILIM-expressing cells. (i) is useful for treating, preventing or ransduction, and for inhibiting the onset and/or advancement of the prophylaxis of delayed type allergy. (i) is useful for treating and prevention and/or treatment of the classes. (i) is useful for suppression, prevention and/or treatment of the classes. (i) is useful for suppression, prevention and/or treatment of the classes. (i) is useful for suppression, prevention and/or treatment of the remarking until in suppression, profit in the and in the suppression, prevention, graft versus pooriasis, autoimmune or allergic disorders, inflammatory dermatosis, pooriasis, autoimmune or allergic disorders, inflammatory disorders caused by abnormal intestinal immunity, specifically inflammatory intestinal disorders such as ulcerative colitis, pneumonia, hepatitis, nephritis, vasculitis, and pancreatitis. (1) induces no serious antifemicity (HAMA) in a host. AAUTA296-AAUTA301 represent anti-mune antigenicity (HAMA) in a host. AAUTA296-AAUTA301 represent anti-human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Osteoprotegerin ligand, osteopathic; antiinflammatory; antirheumatic; antiarthritic; cytostatic; OPGL; anti-OPGL-1; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 METPAQLLFLLLLWLPDTTGEIVLTQFPGTLSLSPGERATLSCRASQSVASAYLAWYQQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89.4%; Score 660; DB 5; L 88.8%; Pred. No. 2.8e-41; ive 8; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l. .20
/note= "IgG2 signal peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note= "variable region"
29. .235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anti-OPGL-1 antibody kappa light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GOGTKLEIKRTVAAPSVFIFPPS 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 88.8
Matches 127; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 236 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-APR-2003
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                                                                                                                                                                                                                                          The invention relates to antibodies that interact with osteoprotegerin ligands (OPGL). The antibody is useful for detecting the level of OPGL in a blological sample. The antibody, or the pharmaceutical composition comprising the antibody, is also useful for treating osteopenic disorder, an inflammatory condition with attendant bone loss, an autoimmune condition with attendant bone loss in a patient or rheumatoid arthritis in a patient. In particular, the antibody or composition is useful for treating bone diseases, e.g. osteoporosis, bone loss from arthritis, byaget's disease, osteopenia, endocrine osteoporosis (e.g. Cushing's syndrome or acromegaly), osteogenesis imperfecta, homocystinutia, Menkes' syndrome, osteomyllitis, hypercalcemia, or osteomyllitis, hypercalcemia, or osteomycone, represents an anti-OPGL-1 antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 PGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVFYCQQYGSSP-RTF 119
                                                                                                                                                                                                                                         with osteoprotegerin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                        New antibodies that interact with osteoprotegerin ligands, useful for treating osteopenic disorders, e.g. osteoporosis, bone loss from arthritis, Paget's disease, osteopenia, osteomyelitis, hypercalcemia and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Monoclonal antibody; variable region; heavy chain; light chain; VH; VL; complementarity determining region; CDR; MAb; BO2C11; conformational peltope; factor VIII; KRIX1; von Willebrand factor; hemostasis; intravascular coagulation; arterial thrombosis; arterial restenosis; venous thrombosis; arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 METPAQLIFILILIMIPDITGEIVLIQSPGTISLSPGERATLSCRASQSVRGRYLAWYQQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 PGQAPRLLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSALLTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 METPAQLLFLLLMLPDTTGBIVLTQFPGTLSLSPGBRATLSCRASQSVASAYLAWYQQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 658.5; DB 6; Length 235;
Pred. No. 3.6e-41;
2; Mismatches 9; Indels 1:
                                              Ω;
                                              Davis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Light chain variable region VL of BO2C11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 GQGTKVEIKRTVAAPSVFIFPPS 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 GGGTKVEIKRTVAAPSVFIFPPS 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                              Corvalan JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB47060 standard; protein; 142 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2,
                                                                                                                                                                                                                Claim 1; Fig 4; 144pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43. .54
/label= CDR1
69. .75
/label= CDR2
109. .117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109. :117
/label= CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89.2%;
91.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 131; Conservative
                                              Boyle WJ, Martin FH,
                                                                                WPI; 2003-210262/20.
(ABGE-) ABGENIX INC. (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                   kappa light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 235 AA;
                                                                                                 N-PSDB; ABZ59148
                                                                                                                                                                                 osteonecrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB47060;
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The present invention relates to a pharmaceutical composition for the prevention and/or treatment of systemic Inflammatory response syndrome (SIRS), sepsis, septic shock, thrombus formation in the microvasculature and disseminated intravascular coagulation in mammals, comprising as an extive inparedient a partial inhibitor of factor VIII, in admixture with a carrier. Such inhibitors may include the antibodies BO2CII and KRIXI. The present sequence is the light chain variable region of BO2CII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 PGQAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYXCQKYGTSA-ITF 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PGQAPRLLIYGASSRATDIPHRPSGSGSTDFTLTISRLEPEDFAVYYCQQYGTSALLTF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system; hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 METPAQLLFILILMLPDTTGEIALTQSPGTLSLSPGERATLSCRASQSFSSSYLAWYQQX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 METPAQLIFILLIMIPDITGEIVLTQFPGTLSLSPGERATLSCRASQSVASAYLAWYQQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pharmaceutical composition for treating systemic inflammatory respons syndrome, sepsis, septic shock and/or thrombus formation in microvasculature in mammals, comprises a partial inhibitor of factor
complementarity determining region; antibacterial; antiinflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match

Best Local Similarity 89.5%; Pred. No. 4.4e-41;
Matches 128; Conservative 7; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The kappa chain of immunoglobulin clone 4.8.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGGTKVEIKRTVAAPSVFIFPPS 143
                                                                      ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 11; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY93704 standard; protein; 233
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                                                                                                                        69...75
/label= CDR2
108..116
/label= CDR3
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                                                                                                                                                                                                                                                                                                                       11-JAN-2001; 2001US-0261405P.
                                                                                                                                                                                                                                                                                                                                                             (COLL-) COLLEN RES FOUND VZW
                                                                                           13. .54
/label≃ CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                  2002-610270/66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAL49255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 142 AA;
                                                                                                                                                                                                                                                                                                                                                                                                 Jacquemin MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-OCT-2000
                                                                                                                                                                                                                  EP1222929-A2
                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
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                                                                                                                              Region
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                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents the light chain variable region of the human monoclonal antibody (MAb), BO2C11. BO2C11 is a human MAb which recognises a conformational epitope within the carboxy-terminal of the factor VIII light chain. BO2C11 recognises both the wild type and Arg2150His factor VIII light chains. The MAb produced by the cell line of the invention, KRIX1, specifically recognises the wild type factor VIII light chain. KRIX1, can be used to inhibit the binding of factor VIII light chain. KRIX1, can be used to inhibit the binding of factor VIII light chain. Cartor in a dose dependant manner. The new cell line KRIX 1, is deposited with the Belgian Coordinated Collections of Micro-organisms, under accession number LMBP 508050E KRIX1, or fragments of it, optionally with a thrombolytic agent, are useful for the treatment and/or prevention of hemostasis, coagulation disorder or thrombosic pathologic condition such as intravascular coagulation, arterial thrombosis, arterial restenosis, venous thrombosis or arteriosclerosis, and attenuation of coagulation in a mammal. An effective and safe antithrombotic therapy is provided which reduces the risk of bleeding in mammals, more particularly in humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PGOAPRLLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSALLTF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; antibody; B02C11; KRIX1; light chain; heavy chain; inflammation; variable region; factor VIII inhibitor; sepsis; septic shock; thrombus formation; systemic inflammatorx esponse syndrome; CDR; disseminated intravascular coagulation; haemophilia A; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 METPAQLIFLILIMIPDITGELALTQSPGTLSLSPGERATLSCRASQSFSSSYLAWYQQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 METPAQLIFILLIMIPDITGEIVLTQFPGTLSLSPGERATLSCRASQSVASAYLAWYQQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                         Novel cell lines for producing monoclonal antibodies that bind to factor involved in hemostasis and coagulation cascade, useful for treating and preventing coagulation disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ٦;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 88.7%; Score 654.5; DB 4; Best Local Similarity 89.5%; Pred. No. 4.4e-41; Matches 128; Conservative 7; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human B02C11 light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGTKVEIKRTVAAPSVFIFPPS 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA018877 standard; protein; 142 AA
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                                                                                                                                                                                                                                                                                                                                                                                  Example 5; Fig 7; 55pp; English
                                                                                                                                                                                                                     Saint-Remy JR;
                                                                                           13-JUL-2000; 2000WO-EP006677
                                                                                                                                                                                 RES & DEV VZW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                        WPI; 2001-138333/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 142 AA;
                                                                                                                                                                                                                                                                         N-PSDB; AAC85453
                                                                                                                                                                                   (LEUV-) LEUVEN
                      WO200104269-A1
                                                                                                                                                                                                                     Jacquemin MG,
                                                                                                                              14-JUL-1999;
14-JUL-1999;
                                                         18-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA018877;
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9

Gaps

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Length 142; Indels Davis CG;

Gilman SC,

WO200037504-A2

Homo sapiens

23-DEC-1999; 23-DEC-1998;

29-JUN-2000

Hanson DC, Corvalan JR;

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The present sequence represents a kappa chain of an antibody of the invention. The antibody is directed cytotoxic T-lymphocyte antigen (CTLA) that bodies of the invention are composed of a heavy chain variable region, comprising a modified contiguous sequence from a FRI-FR3 sequence encoded by a human VH3-33 family gene. The modifications are contained in 10PR1, CDR2 and/or framework regions. The antibodies may be used to inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity disorders (e.g. autoimmune disease, diabetes and graft rejection) and used to up-regulate immune system to up-regulate may be disorders (e.g. cancer). CTLA-4 stimulatory agents may be disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 PGQAPRLLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDRAVYCQQYGTSALLIF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel antibodies capable of binding cytotoxic T-lymphocyte antigen (CTLA) -4 containing specified heavy and light chain sequences, useful for treating, e.g. immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 METPAQLLFLLLLWLPDTTGEIVLTQFPGTLSLSPGERATLSCRASQSVASAYLAWYQQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 METPAQLLPLILLMLPDTTGEIVLTQSPGTLSLSPGERATLSCRT--SVSSSYLAWYQQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; cytotoxic T lymphocyte antigen-4; therapy; CTLA-4 antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 654.5; DB 3;
Pred. No. 7e-41;
2; Mismatches 7;
                                                                                                                                                                                                                                                                                                                       Mueller EE, Hanke JH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human 4.8.1 anti-CTLA-4 antibody kappa chain.
                                                    /note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGGTKVEIKRTVAAPSVFIFPPS 140
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                 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3, Fig 22k; 157pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE35886 standard; protein; 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

Best Local Similarity 91.6%;
Matches 131; Conservative
                                                                                                                                                                                99WO-US030895
                                                                                                                                                                                                                       98US-0113647P
                                                                                                                                                                                                                                                                                                                         Neveu MJ,
                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-442647/38.
N-PSDB; AAA46895.
                                                                                                                                                                                                                                                            (PFIZ ) PFIZER INC. (ABGE-) ABGENIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 233 AA;
                                                                                               WO200037504-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                23-DEC-1999;
                                                                                                                                                                                                                       23-DEC-1998;
                                                                                                                                                                                                                                                                                                                                             Corvalan JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-JUN-2003
                                                                                                                                         29-JUN-2000
                                                                                                                                                                                                                                                                                                                         Hanson DC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118
                     Key
Peptide
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g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a kappa chain of an antibody of the invention. The antibody is directed cytocoxic T-lymphocyte antipled (CTLA) 1. Antibodies of the invention are composed of a heavy chain variable region, comprising a modified contiguous sequence from a FRI-FR3 sequence encoded by a human VH3-33 family gene. The modifications are contained in CDR1, CDR2 and/or framework regions. The antibodies may be used to inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity disorders (e.g. cancer). CTLA-4 stimulatory agents may be used to used it is not an inhibit cancer. CTLA-4 stimulatory agents may be used to up-regulate disorders (e.g. cancer). CTLA-4 stimulatory agents may be used to up-regulate immune system to up-regulate immundeficient
                                                                                                                                                                                                                                                                                                                                                                                                                       Novel antibodies capable of binding cytotoxic T-lymphocyte antigen (CTLA) -4 containing specified heavy and light chain sequences, useful for treating, e.g. immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system; hyperimmunity disorder; autoimmune disease; diabetes; graft rejection; proliferative disorder; cancer; immunodeficient disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 METPAQLLFLLLLLWLPDTTGEIVLTQFPGTLSLSPGERATLSCRASQSVASAYLAWYQQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 METPAQLIFILILIMUPDITGEIVITQSPGTLSLSPGERATLSCRI--SVSSSYLAWYQQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PGOAPRLLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSALLTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGISP-FTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                        Davis CG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 233;
                                                                                                                                                                                                                                                                                                        Gilman SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
proliferative disorder; cancer; immunodeficient disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 654.5; DB 3;
Pred. No. 7e-41;
2; Mismatches 7;
                                                                                                                                                                                                                                                                                               Hanke JH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The kappa chain of immunoglobulin clone 4.8.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGTKVEIKRTVAAPSVFIFPPS 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118 GGGTKVEIKRTVAAPSVFIFPPS 140
                                                                                                                                                                                                                                                                                                        Mueller EE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; Fig 1B; 157pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY93731 standard; protein; 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88.7%;
91.6%;
                                                                                                                                                            99WO-US030895.
                                                                                                                                                                                                      98US-0113647P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 131, Conservative
                                                                                                                                                                                                                                                                                                        Neveu MJ,
                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-442647/38.
N-PSDB; AAA46867.
                                                                                                                                                                                                                                           (PFIZ ) PFIZER INC. (ABGE-) ABGENIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 233 AA;
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disorders

Query Match Local 117

Homo sapiens

03-OCT-2000

SXXXXXXXXXXXXXX

AAY93731;

RESULT 1

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9 58

Gaps

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Indels

Length 233;

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ulcerative colitis; pneumonia; nephritis; vasculitis; pancreatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 236 AA;
                                                                   WO200187981-A2.
                                    Homo sapiens.
                                                                                                    22-NOV-2001
                                                                                                                                                                                                                                                         Tsuji T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
AAW40069
ID AAW40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to the use of human anti-cytotoxic T lymphocyte antigen-4 (anti-TTLA-4) antibody in the preparation of a medicament for the treatment of cancer such as bone cancer, pancreatic cancer, skin cancer, cutaneous or intraocular malignant melanoma, uterine and ovarian cancer, cancer of the anal region, stomach cancer, breast cancer, testicular cancer, uterine cancer and carcinoma of the fallopian tubes. The present sequence is human anti-CTLA-4 antibody kappa chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 METPAQLIFILLIMIPDITIGEIVITQPPGTLSLSPGERATLSCRASQSVASAYLAWYQQK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiallergic; antiulcer; neuroprotective; antithyroid; vasotropic; immunosuppressive; dermatological; antiinflammatory; hepatotropic; activation inducible lymphocyte immunomodulatory molecule; ALLIM, monoclonal antibody; allergy; rheumatoid arthritis; diabetes mellitus; multiple sclerosis; autoimmune thyroiditis; psoriasis; hepatitis; allergic contact-type dermatitis; chronic inflammatory dermatosis; systemic lupus erythematosus; autoimmune disorder; inflammation; graft versus host reaction; immune rejection; intestinal immunity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                          Use of human anti-cytotoxic T lymphocyte antigen-4 antibody in the preparation of medicament for the treatment of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anti-human AILIM monoclonal antibody clone Jmab-139, light chain.
                                                                   21. .233 //note= "Mature anti-CTLA-4 antibody kappa chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88.7%; Score 654.5; DB 6; Length 91.6%; Pred. No. 7e-41; 7; Indels ive 2; Mismatches 7; Indels

    .20
    /label= Signal_peptide

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                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU74301 standard; protein; 236 AA
                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 1K; 76pp; English.
                                                                                                                                                                                         23-MAY-2002; 2002EP-00253652
                                                                                                                                                                                                                          23-MAY-2001; 2001US-0293042P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 131; Conservative
                                                                                                                                                                                                                                                           (PFIZ ) PFIZER PROD INC.
                                                                                                                                                                                                                                                                                            Mueller EE;
                                                                                                                                                                                                                                                                                                                           WPI; 2003-131215/13.
N-PSDB; AAD54346.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 233 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-MAR-2002
                                                                                                                    EP1262193-A1
                                                                                                                                                                                                                                                                                            Hanson DC,
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                                                                     Protein
                                    Peptide
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The invention relates to a novel human antibody (I), preferably a human monoclonal antibody which binds to an activation inducible lymphocyte immunomodulatory molecule (AILIM). (I) is useful for modulating signal transduction into a cell mediated by AILIM, for modulating proliferation of AILIM-expressing cells, for modulating production of a cytokine from AILIM-expressing cells, for inducing antibody-dependent cytokine from against AILIM-expressing cells, (I) is useful for treating, preventing or AILIM-expressing cells. (I) is useful for treating, preventing or preventing, and diseases associated with AILIM-mediated costimulatory transduction, and for inhibiting the onset and/or advancement of the diseases. (I) is useful for suppression, prevention and/or treatment of the antibution, multiple sclerosis, autoimmune cytoimmune thyroiditis, captemic lupus erythematosus, insulin-dependent diabetes mellitus, psortemic lupus erythematosus, insulin-dependent diabetes mellitus, contaction, graft versus host disease, immune rejection, disorders caused by abnormal intestinal immunity, specifically inflammatory inflammatory described and disorders such as ulcerative colitis, pneumonia, hepatitis, nephritis, vasculitis, and pancreatities. (I) induces no serious immune preference of the inflammatory of the inflammatory of the inflammatory of intestinal disorders such as ulcerative colitis, pneumonia, hepatitis, and pancreatitis. (I) induces no serious immune colitically inflammatory of antigenicity to human i.e., human anti-mouse immunorejection due to antigenicity to human, i.e., human anti-human contribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 PGQAPRLLIYGASSRATDIPHRESGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSALLTF 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New human monoclonal antibody that binds to activation inducible lymphocyte immunomodulatory molecule, useful for treating rheumatoid arthritis, multiple sclerosis and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AILIM monoclonal antibody amino acid sequences of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match

88.3%; Score 652; DB 5; length 23
Best Local Similarity 88.1%; Pred. No. 1.1e-40;
Matches 126; Conservative 9; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 30; Page 298-299; 300pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 GGGTKVEIKRTVAAPSVFIFPPS 143
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                                                                                               18-MAY-2000; 2000JP-00147116.
30-MAR-2001; 2001JP-00099508.
15-MAY-2001; 2001WO-JP004035
                                                                                                                                                                                                                                                    (NISB ) JAPAN TOBACCO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                              WFI; 2002-075313/10.
N-PSDB; AAS99477.
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AAW40069;

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This sequence represents the human Hil monoclonal antibody variable (V) region heavy (H) chain which specifically recognises the C-antigen. Such an antigen binding fragment may be used for treating a patient with neoplasia. It is especially useful in the detection of lymphomas and leukaemias where the tumour cells bearing the C antigen are circulating in the patients bloodstream. The polymucleotide sequence may be used as a primer or a probe and the encoded protein may be used in a vaccine or for gene therapy. The human monoclonal antibody (Wab), designated Hil, specifically recognises cancerous cells. Hil is specific for specifically recognises cancerous cells. Hil is specific for glioblastoma, neuroblastoma, mailgnant melanoma, breast adenocarcinoma, lung adenocarcinoma, anall cell lung carcinoma, colon adenocarcinoma and prostate adenocarcinoma. The antigen binding fragment may also be used to detect C-antigen in a sample
                                                                                                            H11; monoclonal antibody; MAD; C-antigen; variable region heavy chain; V region; H chain; neoplasia; detection; Jymphoma; tumour call; probe; primer; vaccine; gene therapy; glioblastoma; neuroblastoma; malignant melanoma; adenocarcinoma; small cell lung carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antigen binding fragment from monoclonal antibody, H11 - allows tumour specific detection and treatment of neoplasia.
                                                                         Human monoclonal antibody H11 protein variable region H chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 87-88; 126pp; English
                                                                                                                                                                                                                                                                                                                                                                                                     (NOVO-) NOVOPHARM BIOTECH INC
                                                                                                                                                                                                                                                                                                                            97WO-US008962,
                                                                                                                                                                                                                                                                                                                                                                96US-00657449.
                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-018515/02.
N-PSDB; AAV10111.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Maiti PK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 150 AA;
                                                                                                                                                                                                                                              WO9744461-A2
                                                                                                                                                                                                                                                                                                                            22-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                  22-MAY-1996;
                                                                                                                                                                                                              Homo sapiens
                                      29-MAY-1998
                                                                                                                                                                                                                                                                                     27-NOV-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Dan MD,
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                                                                                                                1 METPAQLIFILLIMIPDITGEIVLIQFPGTISLSPGERATISCRASQSVASAYLAWYQQK
Query Match 88.0%; Score 649.5; DB 2; Length 150;
Best Local Similarity 87.7%; Pred. No. 1.1e-40;
Matches 128; Conservative 7; Mismatches 8; Indels 3; Gaps
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61 PGQAPRLLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTS---AL 117 65 PGQAPRILIYGASTRATGMPDRFSGSGSGTDFTLTISRLEPEDFAVYCQQYGSSPQTPQ 124 5 MEPÇAQLIFILLILMIPDITGDIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQK 64 g d ò

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Search completed: April 5, 2004, 13:24:17 Job time : 46.2149 secs

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April 5, 2004, 13:42:12 ; Search time 33.6328 Seconds (without alignments) 1116.513 Million cell updates/sec
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738
1 METPAQLIFLILLMLPDTTG.....TKVEIKRTVAAPSVFIFPPS 143
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1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/NEG_NEW PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/USO6_NEW PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO6_NEW PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*
7/cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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14: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                            OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                         Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	Sequence 8, Appli	Sequence 7, Appli	Sequence 34, Appl	Sequence 4, Appli		Sequence 11, Appl	Sequence 38, Appl	Sequence 5, Appli		Sequence 237, App	Sequence 95, Appl	Sequence 89, Appl	Sequence 91, Appl	Sequence 93, Appl	Seguence 4, Appli
SUMMARIES	qı	US-10-044-569B-8	US-10-153-382-7	US-09-859-053-34	US-10-180-648-4	US-10-044-569B-4	US-10-153-382-11	US-09-859-053-38	US-09-782-397-5	US-10-153-382-15	US-09-833-245-237	US-10-309-762-95	US-10-309-764-89	US-10-309-762-91	US-10-309-762-93	US-09-848-832-4
	DB	14	14	σ	12	14	14	σ	10	14	11	15	15	15	15	10
	% Query Match Length DB	143	235	236	235	142	233	236	150	234	236	127	128	127	127	234
	% Query Match	100.0	90.3	89.4	89.2	88.7	88.7	88.3	88.0	87.4	82.5	80.8	80.4	80.4	80.2	79.3
	Score	738	666.5	9	658.5	654.5	654.5	652	649.5	645	609	596	593.5	593	592	585
	Result No.		7	m	4	Ŋ	ø	7	œ	o.	10	11	12	13	14	15

Sequence 4, Appli	(S)	9	9 8	equence 806,	807	42,	50,	986	eo eo	e 52,	72,	Sequence 122, App	38,	335	334,	equence 74,	121	105,	76,	equence 49;	equence 141,	equence 44,	equence 78,	Sequence 107, App	107	e 97,	•	-	101
US-10-225-108A-4	US-10-461-14	US	US-10-291-26	US-10-291-265-80	US-10-291-265-807	US-09-453-234-4	US-09-453-234-50		US-09-453-234-	US-09-453-234-5	US-09-453-234-7	US-10-307-72	US-09-453-234-3		US-10-291-26	US-09-453-234-7	US-10-309-76	US-10-309-76	US-09-453-234-76	US-09-791-1	US-10-30	US-09-453-		US-10-216-484-107		US-10-309-76	US-09-453-2	US-10-443-466A-25	US-10-309-764-101
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ALIGNMENTS

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DEPLICANT: D. Collen Research Foundation vzw
APPLICANT: D. Collen Research Foundation vzw
APPLICANT: Jacquemin, Marc G
APPLICANT: Saint-Remy, Jean-Marie R
APPLICANT: Saint-Remy, Jean-Marie R
APPLICANT: Saint-Remy, Jean-Marie R
TITLE OF INVENTION: Method and pharmaceutical composition for preventing
TITLE OF INVENTION: Method and pharmaceutical composition for preventing
TITLE TEPERENCE: C1968
CURRENT APPLICATION NUMBER: 2010-01-11
PRIOR APPLICATION NUMBER: US 60/261,405
PRIOR PILING DATE: 2001-01-11
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.1
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
) LOCATION: (325)...(354)
) CTHER INFORMATION: complementary determining region number three
1S-10-044-569B-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PORTURE:
NAME/KEY: misc feature
LOCATION: (127)...(162)
OTHER INFORMATION: complementary determining region number one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            number two
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NAME/KEY: misc_feature
LOCATION: (205)..(225)
OTHER INFORMATION: complementary determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 738; DB 14; Best Local Similarity 100.0%; Pred. No. 1.7e-56; Matches 143; Conservative 0; Mismatches 0;
                     Sequence 8, Application US/10044569B Publication No. US20030175268A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 143
TYPE: PRT
ORGANISM: Homo sapiens
US-10-044-569B-B
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Gaps

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Length 143; Indels

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; ORGANISM: Mus musculus US-10-180-648-4
           ; ORGANISM: Homo sapiens
US-09-859-053-34
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Best Local Similarity
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US-10-044-569B-4
TYPE: PRT
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                                                                                  61 PGQAPRILIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSALLTF 120
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                                                                PGOAPRLLIYGASSRATDIPHRFSGSGTDFTLTISRLEPEDFAVXYCQOYGTSALLTF 120
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                                      1 METPAQILFLLILMLPDTTGEIVLTQFPGTLSLSPGERATLSCRASQSVASAYLAWYQQK
              1 METPAQLLFLLLLWLPDTTGEIVLTQFPGTLSLSPGERATLSCRASQSVASAYLAWYQQK
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Pred. No. 4.6e-50;
5; Mismatches 6; Indels 1;
                                                                                                                                                                                                                                                      APPLICANT: PFIZER PRODUCTS INC.
TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
FILE REFERENCE: PC23019A
CURRENT APPLICATION NUMBER: US/10/153,382
CURRENT PILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: 60/293042
PRIOR FILING DATE: 2001-05-23
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PATENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 GGGTKVEIKRTVAAPSVFIFPPS 143
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                                                                                                                    121 GGGTKVEIKRTVAAPSVFIFPPS 143
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Publication No. US20030086930A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             90.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 91.6
Matches 131; Conservative
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CORGANISM: Homo sapiens
US-10-153-382-7
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US-09-859-053-34
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Sequence 4, Application US/10044569B;
Publication No. US20030175268A1;
GENERAL INFORMATION:
APPLICANT: D. Collen, Marc G
APPLICANT: Saint-Remy, Jean-Marie R
TITLE OF INVENTION: Method and pharmaceutical composition for preventing
TITLE OF INVENTION: and/or treating systemic inflammatory response syndrome
FILE REFERENCE: C1968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 PGQAPRILLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSALLTF 120
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                                                                                                                                                                                                            61 PGQAPRLLIYGASSRATDIPHRESGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSALLTF 120
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  Length 236;
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                                                   8; Indels
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Pred. No. 2.2e-49;
2; Mismatches 9
89.4%; Score 660; DB 9;
88.8%; Pred. No. 1.7e-49;
ive 8; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/10180648
Sequence 4, Application US/10180648
Publication No. US20040033535A1
GENERAL INFORMATION:
APPLICANT: Boyle, William J
APPLICANT: Doyle, William J
APPLICANT: Doyle, William J
APPLICANT: Davis, C. Geoffrey
TITLE OP INVENTION: Antibodies to OPGL
FILE REFERENCE: 06643.0049-00000
CURRENT APPLICATION NUMBER: US/10/180,648
CURRENT FILING DATE: 2002-10-25
PRIOR APPLICATION NUMBER: 60/301,172
PRIOR APPLICATION NUMBER: 60/301,172
PRIOR FILING DATE: 2001-06-26
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3:1
SEQ ID NO 4
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CURRENT APPLICATION NUMBER: US/10/044,569B
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91.6%;
  Query Match
Best Local Similarity 88.8 Matches 127; Conservative
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118 GGGTKVEIKRTVAAPSVFIFPPS 140

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61 PGQAPRILIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSALLTF 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 PGQAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEFBDFAVYCQKYGTKGTSA-ITF 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 PGQAPRILIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSALLTF 120
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LOCATION: (325)..(351)
OTHER INFORMATION: complementary determining region number three
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 654.5; DB 14; Length 233; Pred. No. 4.9e-49; 2; Mismatches 7; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88.7%; Score 654.5; DB 14; Length 142; 89.5%; Pred. No. 2.9e-49; tive 7; Mismatches 7; Indels 1;
                                                                                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (127)...(162)
OTHER INFORMATION: complementary determining region number one
                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature
LOCATION: (205)..(225)
OTHER INFORMATION: complementary determining region number two
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Publication No. US20030086930A1

GENERAL INFORMATION:
APPLICAMINE PETZER PRODUCTS INC.
TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
FILE REFERENCE: PC2019A
CURRENT APPLICATION NUMBER: US/10/153,382
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: 60/293042
PRIOR APPLICATION NUMBER: 60/293042
PRIOR PILING DATE: 2001-05-23
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.1
PRIOR APPLICATION NUMBER: US 60/261,405; PRIOR FILING DATE: 2001-01-11; NUMBER OF SEQ ID NOS: 8; SOFTWARE: Patentin version 3.1; SEQ ID NO 4; LENOTH: 142
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91.6%;
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Best Local Similarity 91.6
Matches 131; Conservative
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Best Local Similarity 89.5
Matches 128; Conservative
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CRGANISM: Homo sapiens
US-10-153-382-11
                                                                                                                                                                                                          ORGANISM: Homo sapiens
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LENGTH: 233
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Sequence 38, Application US/09859053

Patent No. US200201026581

GENERAL INFORMATION:

APPLICANT: Teuji, Takashi

APPLICANT: Teuji, Takashi

TILLE OF INVENTION: US20020103658Aluaki

TILLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A

TILLE OF INVENTION: HARMACEUTICAL USE THEREOF

TILLE OF INVENTION: HARMACEUTICAL USE THEREOF

TILLE OF INVENTION: US0020103658Aluaki

CURRENT APPLICATION NUMBER: US/09/859,053

CURRENT APPLICATION NUMBER: US/09/859,053

PRIOR FILING DATE: 2001-03-30

PRIOR FILING DATE: 2001-03-30

PRIOR FILING DATE: 2001-05-18

NUMBER OF SEQ ID NOS: 43

SOFFWARE: FREEEER FREEEER FREEEER FREEEER FREEEER FREEEER FREEEER FREEEER FREEEER FREEEER FREEEER FREEEER FREEEER FREEEER FREEEER FREEEER FREEEER FREEEER FREEEER FREEEER FREEEER FREEER FREEEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FREEER FR
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FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
DETECTION OF CANCERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PGGAPRLLIYGASSRATDIPHRPSGSGGTDFTLTISRLEPEDFAVYYCQQYGTSALLTF 120
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Kaplan, Howard A.
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 236;
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ZIP: 94304-1018
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88.3%; Score 652; DB 9; L
88.1%; Pred. No. 8.3e-49;
iive 9; Mismatches 8;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster LLP
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 GGGTKVEIKRTVAAPSVFIFPPS 143
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Publication No. US20030021779A1
GENERAL INFORMATION:
APPLICANT: Dan, Michael D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 88.1
Matches 126; Conservative
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US-09-859-053-38
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US-09-782-397-5
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE LOCATION: (117) OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION: (122)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-833-245-237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MEXPAQLIFILILWIPDTTGEIVLTQSPXTLSLSPGERATLSCRASQSV-SSYLAWYQQK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 METPAQLLFLLLMLPDTTGEIVLTQFPGTLSLSPGERATLSCRASQSVASAYLAWYQQK
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                                                                                                                                                                                                                   TITLE OF INVENTION: Albumin Fusion Proteins
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF546PCT
CURRENT APPLICATION NUMBER: US/09/833,245
CURRENT FILING DATE: 2001-04-12
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/256, 931
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/199, 384
PRIOR APPLICATION NUMBER: 60/199, 384
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SEQ THARE: PATCHIN VOR: 2267
SEQ THARE: PATCHIN VOR: 2267
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; Sequence 237, Application US/09833245; Publication No. US20040010134A1; GENERAL INFORMATION:
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Best Local Similarity 86.8 Matches 125, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (3)
OTHER INFORMATION: Xaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
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US-09-833-245-237
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Sequence 15, Application US/10153382

Publication No. US20030086930A1

GENERAL INFORMATION:
APPLICANT: PFIZER PRODUCTS INC.
ITILE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
FILE REFERENCE: PC23019A

CURRENT FILING DATE: 2002-05-22

PRIOR APPLICATION NUMBER: US/10/153,382

CURRENT FILING DATE: 2001-05-23

NUMBER OF SEQ ID NOS: 39

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 15

LENGTH: 234
                        FILING DATE: 13-Feb-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/862,124
FILING DATE: 1997-05-22
ATTORNEY AGENT INFORMATION:
NAME: Lebnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFRENCE/DOCKET NUMBER: 31608-20001.20
TELECHONE: (650) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 88.0%; Score 649.5; DB 10; Best Local Similarity 87.7%; Pred. No. 8.4e-49; Matches 128; Conservative 7; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 645; DB 14;
Pred. No. 3.3e-48;
2; Mismatches 9;
        APPLICATION NUMBER: US/09/782,397
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SEQUENCE DESCRIPTION: SEQ ID NO: 5:
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                                                                                                                                                                                                                                                                                                                        TELEX: 706141
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHRACTERISTICS:
LENGTH: 150 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 90.9%;
Matches 130; Conservative
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ORGANISM: Homo sapiens
US-10-153-382-15
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61 PGQAPRILLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSALLTF 120
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                                                              61 PGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYHCQQYG-STPLTF 119
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                                                                                                                                                                                                                                                                                                               RESULT 13
US-10-309-762-91
i Sequence 91, Application US/10309762
i Publication No. US20040018198A1
i GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gudas, Jean
APPLICANT: Handa, Manahisa
APPLICANT: Gallo, Michael
APPLICANT: Gallo, Michael
APPLICANT: MICHON MICHON STREAM
APPLICANT: MICHON MICHON STREAM
APPLICANT: MICHON STREAM
APPLICANTION: (CA IX) TUMOR ANTIGEN
FILE REFERENCE: ABGENIX: 027A
CURRENT APPLICATION NUMBER: 00/1309,762
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/337275
PRIOR APPLICATION NUMBER: 60/337275
PRIOR APPLICATION NUMBER: 60/337275
ANTHER FERSON STREAM
CURRENT FILING DATE: 2001-12-03
ANTHER OF SEQ ID NOS: 246
SEQ ID NO 91
LENGTH: 127
TYPE: PRI
APPE: PRI
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Publication No. US20040018198A1

GENERAL INFORMATION:
APPLICANT: Gands, Jean
APPLICANT: Foltz, Ian
APPLICANT: Boltz, Ian
APPLICANT: Ballo, Michael
ITLE OF INVENTION: (A IX) TUMOR ANTIGEN
FILE REFERENCE: ABGENIX. 0.27A
CURRENT APPLICATION NUMBER: US/10/309,762
CURRENT FILING DATE: 2002-12-02
FRIOR APPLICATION NUMBER: 60/337275
FRIOR APPLICATION NUMBER: 60/337275
FRIOR APPLICATION NUMBER: 60/337275
FRIOR APPLICATION NUMBER: 60/337275
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FRIOR APPLICATION NUMBER: 60/337275
FRIOR APPLICATION NUMBER: 60/337275
FRIOR APPLICATION NUMBER: 1201-12-03

INUMBER OF SEQ ID NOS: 246
SEQ ID NO 93

LENGTH: 127
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ORGANISM: Homo sapiens
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US-10-309-762-93
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US-10-309-764-89
Sequence 89, Application US/10309764
Sequence 89, Application No. US20030232009a1
Sequence 89, Application No. US20030232009a1
Septence No. US20030232009a1
Septence No. US20030232009a1
Septence No. US20030232009a1
Septence No. US2002, Ian
APPLICANT: Balathumpat, Raju
APPLICANT: Selathumpat, Raju
APPLICANT: Yang, Xiao-dong
APPLICANT: Yang, Xiao-dong
APPLICANT: Wang, Xiao-dong
TILLE OF INVENTION: TREATING AUTOIMMUNE DISEASE AND TRANSPLANT REJECTION
TILLE OF INVENTION: TREATING AUTOIMMUNE DISEASE AND TRANSPLANT REJECTION
TILLE OF INVENTION NUMBER: 00/337,276
CURRENT APPLICATION NUMBER: 60/337,276
PRIOR FILLNG DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 147
SEQ ID NO 89
LENGTH: 128
LENGTH: 128
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80.4%; Score 593.5; DB 15; Length 128;
Best Local Similarity 91.5%; Pred. No. 5.1e-44;
Matches 118; Conservative 3; Mismatches 7; Indels 1;
                       US-10-309-762-79

Sequence 95, Application US/10309762

Publication No. US20040018198A1

Fublication No. US20040018198A1

Fublication No. US20040018198A1

APPLICANT: Gudas, Jean

APPLICANT: Foltz, Ian

APPLICANT: Gallo, Michael

TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX

TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX

TITLE OF INVENTION: (ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX

TITLE OF INVENTION: (ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX

FILE REFERENCE: ABGENIX.027A

CURRENT APPLICATION NUMBER: 0202-12-02

FRIOR FILING DATE: 2002-12-03

FRIOR FILING DATE: 2001-12-03

NUMBER OF SEQ ID NOS: 246

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 95

LENGTH: 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

80.8%; Score 596; DB 15; Length 127;
Best Local Similarity 91.5%; Pred. No. 3.1e-44;
Matches 118; Conservative 2; Mismatches 7; Indels
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US-10-309-764-89
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US-10-309-762-95
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Gaps 5

US-10-309-762-93

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Sequence 4, Application US/09648832
; Sequence 4, Application US/09648832
; Sequence 4, Douglas
; Publication No. US20030165507A1
; GENERAL INFORMATION:
    APPLICANT: Hooper, Douglas
; APPLICANT: Dietzschold, Bernhard
; TITLE OF INVENTION: RABIES VIROS-SPECFIC NEUTRALIZING HUMAN
    TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND NUCLEIC ACIDS AND RELATED METHODS
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND NUCLEIC ACIDS AND RELATED METHODS
; TITLE OF INVENTION NUMBER: US/09/848,832
CURRENT APPLICATION NUMBER: 00/204,518
PRIOR PLING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PastSEQ for Windows Version 4.0
; SEQ ID NO 4
LENGTH: 234
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79.3%; Score 585; DB 10; Length 234;
Best Local Similarity 83.9%; Pred. No. 5.3e-43;
Matches 120; Conservative 5; Mismatches 16; Indels
Query Match

80.2%; Score 592; DB 15; Length 127;
Best Local Similarity 90.7%; Pred. No. 6.8e-44;
Matches 117; Conservative 2; Mismatches 8; Indels 2
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